

```

Db      235 KLEPSCGPTSTINPCPCKECHKCPAPMLEGSPSEFIPPEIKDVLMLSLPKVYCVYVDV 294
Qy      294 SHEDPEVKFMVYDGVYHNAAKTRPREOYNSTRVAVSVLTVLHODMLNGKEKCKYSNK 353
Db      295 SEDPDVQISWFMVYNNVEVLTAAQTOTHRREDYNSTRVAVSLPIQODMMSKEFEKCKVNNK 354
Qy      354 ALPAPIEKTISKAKGPREPOVYTLPPREEMTKNOYSLTCLVKGFPDIAVEMESNGQ 413
Db      355 DLPAPIERTISKIKGIYRAPOVYTLSPPEQLSKVDVSLTCLAVGSPEDISVEMTSNGH 414
Qy      414 PENNYKTTTPVLDSDGSFFLYSKLTVDKSRMOGANNFSCSVMEALHNNHYTOKSLSPG 473
Db      415 TEENYKDTAPVLDSDGSFFLYSKLTVDKSRMOGANNFSCSVMEALHNNHYTOKSLSPG 474
Qy      474 K 474
Db      475 K 475

```

## RESULT 14

```

147159
Ig gamma 2a chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: I47159
R:Kacskovics, I.; Sun, J.; Butler, J. E.
J. Immunol. 153, 3565-3573, 1994
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
A:Reference number: I47158; MUID:95015845; PMID:7930579
A:Accession: I47159
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-328 <KAC>
A:Cross-references: EMBL:U03779; NID:9433123; PIDD:AA52217.1; PID:9433124
C:Gene: IgG2a
C:Superfamily: Immunoglobulin C region; Immunoglobulin homology
F:133-202/Domain: Immunoglobulin homology <IMM>

```

```

Query Match      50.4%; Score 1267; DB 2; Length 328;
Best Local Similarity 69.9%; Pred. No. 1.6e-66;
Matches 232; Conservative 42; Mismatches 52; Indels 6; Gaps 2;

Qy      145 ASTKGSPVFPPLAPSSKSTSGTAAGCLVADYFPEPVTVMSNGALTSGYHTFPAYLQSS 204
Db      1  APTKAPLVYPLAPCGRTSGPNVALGCLASYPPEPVTVWNSGALTSGYHTFPAYLQPS 60
Qy      205 GLYSLSSVTVVPSSSLCTQTYICNVNHPNTKVDKRVKREKSCDKTHTCPCPAPELLGG 264
Db      61  GLYSLSSMVTVPASSLSKSYTCNVNHPATTTKVDKRVGTRKPPCPICPACESP---G 116
Qy      265 PSVFLEPPPKRDLMTSRPEVTCVYVDVSHEDPEVKFNNYVGVGVYHNAAKTRPREOYN 324
Db      117 PSVFLEPPPKRDLMTSRPOVTCVYVDVSOENPEVOFSWYVGVGVYHNAAKTRPREOYN 176
Qy      325 STRVAVSVLTVLHODMLNGKEKCKVSNKALPAPIEKTISKAKGPREPOVYTLPPSREE 384
Db      177 STRVAVSVLTPIQODMLNGKEFKCKVNNKDLPAPIITLISKAKGQTRPOVYTLPPHAE 236
Qy      385 MTKNOVSLTCLVKGFPDIAVEMESNGQ--PENNYKTTTPVLDSDGSFFLYSKLTVDKS 442
Db      237 LSRKSVSITCLVIGFPPDIDVEMQRNGQPEPEGNRYRTTPOQDVGDGYFLYSKFSYDKA 296
Qy      443 RMOGANNFSCSVMEALHNNHYTOKSLSPGK 474
Db      297 SMOGGGIFQCAVMEALHNNHYTOKSLSPGK 328

```

## RESULT 15

```

147160
Ig gamma 2b chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)

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```

C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: I47160
R:Kacskovics, I.; Sun, J.; Butler, J. E.
J. Immunol. 153, 3565-3573, 1994
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of
A:Reference number: I47158; MUID:95015845; PMID:7930579
A:Accession: I47160
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-328 <KAC>
A:Cross-references: EMBL:U03780; NID:9433125; PIDD:AA5218.1; PID:9433126
C:Gene: IgG2b
C:Superfamily: Immunoglobulin C region; Immunoglobulin homology
F:133-202/Domain: Immunoglobulin homology <IMM>

```

```

Query Match      50.2%; Score 1261; DB 2; Length 328;
Best Local Similarity 69.6%; Pred. No. 3.5e-66;
Matches 231; Conservative 41; Mismatches 54; Indels 6; Gaps 2;

```

```

Qy      145 ASTKGSPVFPPLAPSSKSTSGTAAGCLVADYFPEPVTVMSNGALTSGYHTFPAYLQSS 204
Db      1  APTKAPLVYPLAPCGRTSGPNVALGCLASYPPEPVTVWNSGALTSGYHTFPAYLQPS 60
Qy      205 GLYSLSSVTVVPSSSLCTQTYICNVNHPNTKVDKRVKREKSCDKTHTCPCPAPELLGG 264
Db      61  GLYSLSSMVTVPASSLSKSYTCNVNHPATTTKVDKRVGTRKPPCPICPACESP---G 116
Qy      265 PSVFLEPPPKRDLMTSRPEVTCVYVDVSHEDPEVKFNNYVGVGVYHNAAKTRPREOYN 324
Db      117 PSVFLEPPPKRDLMTSRPOVTCVYVDVSOENPEVOFSWYVGVGVYHNAAKTRPREOYN 176
Qy      325 STRVAVSVLTVLHODMLNGKEKCKVSNKALPAPIEKTISKAKGPREPOVYTLPPSREE 384
Db      177 STRVAVSVLTPIQODMLNGKEFKCKVNNKDLPAPIITLISKAKGQTRPOVYTLPPHAE 236
Qy      385 MTKNOVSLTCLVKGFPDIAVEMESNGQ--PENNYKTTTPVLDSDGSFFLYSKLTVDKS 442
Db      237 LSRKSVSITCLVIGFPPDIDVEMQRNGQPEPEGNRYRTTPOQDVGDGYFLYSKFSYDKA 296
Qy      443 RMOGANNFSCSVMEALHNNHYTOKSLSPGK 474
Db      297 SMOGGGIFQCAVMEALHNNHYTOKSLSPGK 328

```

```

Search completed: September 12, 2003, 13:04:25
Job time : 37.4831 secs

```

```

A>Status: preliminary
A:Molecule type: mRNA
A.Residues: 1-474 <RTS>
A.Cross-references: EMBL:X67210, MID:g54826, PIDN:CAG47649.1, PID:g54827
R.Yamawaki-Kataoka, Y.; Kataoka, T.; Takahashi, N.; Obata, M.; Honjo, T.
Nature 283, 786-789, 1990
A.Title: Complete nucleotide sequence of immunoglobulin gamma2b chain gene cloned from r
A.Reference number: A02157; MUID:80120716; PMID:6766534
A.Contents: a allele
A.Accession: A02157
A.Molecule type: DNA
A.Residues: 138-161, 'U', 163-189, 'FP', 193-474 <YAM>
A.Cross-references: GB:j00461
A.Note: the sequence was determined from the germ-line gene
R.Tucker, P.W.; Marcu, K.B.; Slightom, J.L.; Blattner, F.R.
Science 206, 1299-1303, 1979
A>Title: Structure of the constant and 3' untranslated regions of the murine gamma2b hee
A.Reference number: A26235; MUID:80081501; PMID:117548
A.Contents: MPC 11
A.Accession: A26235
A.Molecule type: mRNA
A.Residues: 138-172, 'P', 174-189, 'FP', 193-376, 'T', 378-474 <TUL>
A>Note: Lys-474 is probably removed posttranslationally
R.Tucker, P.W.; Marcu, K.B.; Newell, N.; Richards, J.; Blattner, F.R.
Science 206, 1303-1306, 1979
A>Title: Sequence of the cloned gene for the constant region of murine gamma2b immunogl
A.Reference number: A26232; MUID:80081502; PMID:117549
A.Accession: A26232
A.Molecule type: DNA
A.Residues: 138-172, 'P', 174-189, 'FP', 193-376, 'T', 378-474 <TUS>
R.Ollo, R.; Rougeon, F.
Nature 286, 761-763, 1982
A>Title: Mouse immunoglobulin alpha types: post-duplication divergence of gamma2a and gamm
A.Reference number: A26233; MUID:82173203; PMID:6803173
A.Contents: b allele
A.Accession: A26233
A.Molecule type: DNA
A.Residues: 138-161, 'U', 163-189, 'FP', 193-300, 'R', 302-331, 'A', 333-437, 'DI', 440-474 <OLL>
A.Cross-references: GB:J00461
R.Kim, H.; Yamaguchi, Y.; Masuda, K.; Matsunaga, C.; Yamamoto, K.; Irimura, T.; Takahas
J. Biol. Chem. 269, 12345-12350, 1994
A>Title: O-glycosylation in hinge region of mouse immunoglobulin G2b.
A.Reference number: A53598; MUID:94216359; PMID:7512967
A.Accession: A53598
A.Status: preliminary
A:Molecule type: protein
A.Residues: 234-251 <KIM>
C.Comment: The a allele sequence is shown.
C.Genetics:
A.Introns: 138/1, 236/1, 258/1, 368/1
C.Complex: An immunoglobulin heterotetramer subunit consists of two identical light (Kap)
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C.Superfamily: Immunoglobulin C region; immunoglobulin homology
C.Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobuli
F.157-222/Domain: immunoglobulin homology <IMI>
E.236-257/Region: hinge
F.281-350/Domain: immunoglobulin homology <IM2>
F.387-454/Domain: immunoglobulin homology <IX3>
F.152/Disulfide bonds: interchain (to light chain) #status predicted
F.164-220, 288-348, 394-452/Disulfide bonds: #status predicted
F.247, 250, 253, 256/Disulfide bonds: Interchain (to heavy chain) #status predicted
F.324/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match          56.4%; Score 1417; DB 1: Length 474;
Best Local Similarity 55.5%; Pred No. 4.8e+75;
Matches   267; Conservative    76; Mismatches 124; Indels     14; Gaps      3;

Oy  1 MEFGISWFLVALIKGYACEVQLLESGGGLQVPGSSLRLSCASGFSTFSNYMSVRARP 60
|| : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : 
Db  1 MEMSWIFELFDLTGTACGVHSEVLQQSGPELVNPVGASVMSCAKSATPTTYMMHWKKRP 60
||||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : 

        GGLENVAVSAISGSHTADSVKGRTIISDNSKNITLYLOMNSIAEDTPATYYCAKDRE 120
||||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : 

```

	Query Match	55.7%	Score 1401.5	DB 2	Length 475
Db	61	GQGLEMGVYINPNKDGRKFNKFKGKATLTISDKSSNAYMELSLTSEDAVYVCARDYD	120		
Qy	121	VTMTVLVNGDFWGGQGRVTYVSASSTKGBSPVFLPADSKSTSGTALCLVKDYFPEP	180		
Db	121	YDM-----FAYMGQGLTYVTSAAKTTTPSPVYPLAAGCGDDTGTSSVTSGCLVKGYPES	173		
Qy	181	VTVMWNSGALTSYHTFPVALQSSGLYSLSVYVVPSSSLGTORYTGNVHKHPSNTFYVDK	240		
Db	174	VTVMWNSGSLSSVSHYTLQSALQGLYTMSSSVYVPSSTPMSQYVTCVSVAHPASSTYVDK	233		
Qy	241	RVEPKSCDKT--HTCP-----CPAPELLGSPVFLPPKPKDITLMTSRPEVYCVVDY	293		
Db	234	KLEPSGPISTINPCRPCKECHKCAPNLNEGSPSFIITPPNKTQVLMISLTLPKTYCVVDY	293		
Qy	294	SHEDPEVKFNNYVDGVEVHNNAKTRPREQYVNSTYRVVSVLTVLHQMVLNGEKYCKVSNK	353		
Db	294	SEDDPDVYISFVNANVEHTAQOTQTHREDYVNSTIRVYSTLPIDQHDMWNGKEFKCVNNK	353		
Qy	354	ALPAPIETKTIKAKGQPREPOVYITLPPSRREEMTINQVSLTCLVKGFTFPDIAVWENSGQ	413		
Db	354	DLPSPIETKTIKIGLVRAAPQVYITLPPAPDLSEKRDVSLCLVGVFNPGDISVEMTISNGH	413		
Qy	414	PENNYKTPTPVPLVDSGSPFLYSKTLVYVKSROQGNVPSCSVMHEALNNHTOKSLSLSPG	473		
Db	414	TEENYKTDTPVPLVDSGSTFIITSKLNMKTSKMEKIDTDFSCVNRHGLNXYLTKTISNSPG	473		
Qy	474	K 474			
Db	474	K 474			
RESULT 13					
S01321					
Ig gamma-2b chain precursor - mouse					
C:Species: Mus musculus (house mouse)					
C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 23-Jul-1999					
C:Accession: S01321					
R:De Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Piers, W.					
Eur. J. Biochem. 176, 287-295, 1988					
A:Title: Expression in non-T lymphoid cells of mouse recombinant immunoglobulin directed					
A:Reference number: S01320; MUID:88329081; PMID:318116					
A:Accession: S01321					
A:Molecule type: mRNA					
A:Residues: 1-475 <DEL>					
A:Cross-references: EMBL:X13188; NID:951780; PIDN:CAA31580.1; PID:951781					
A>Note: This sequence was determined from the differentiated gene					
C:Superfamily: Immunoglobulin C region; Immunoglobulin homology					
C:Keywords: Immunoglobulin					
F:1-19/Domain: Signal sequence #status predicted <SIG>					
F:20-475/Product: Ig gamma-2b chain #status predicted <MAT>					
F:159-223/Domain: Immunoglobulin homology <IMM>					
Query Match	55.7%	Score 1401.5	DB 2	Length 475	
Best Local Similarity	55.3%	Pred. No. 3.8e-74			
Matches 266; Conservative 82; Mismatches 120; Indels 13; Gaps 4;					
Qy	1	MEFGLSWFLVAIIKGVQCEYQLESGGLVQPGSLRLSCAASGFTFSNYAMSWYPOAP	60		
Db	1	MEMIWIIFLILSGTAGVQSQVQLOQSGAELARPAASVAKLSCKASGYITLTSGISWVQRT	60		
Qy	61	GKGLEWVASIASGSHSTYLDVSKGRFTISRDNSKNTLYIQMNSLRADETAVYCAKDRE	120		
Db	61	GQGLEWVGEIETPGSGNSYFNEKFKGKATLTFLDKSSYATVYHLTSLTSEDAVYFCAPRQ	120		
Qy	121	VTMTVLVNGDFWGGQGRVTYVSASSTKGBSPVFLPADSKSTSGTALCLVKDYFPEP	180		
Db	121	VGLL-----PGYVGQGLTYVTSAAKTTTPSPVYPLAAGCGDDTGTSSVTGLCLVKGYPES	175		
Qy	181	VTVMWNSGALTSYHTFPVALQSSGLYSLSVYVVPSSSLGTORYTGNVHKHPSNTFYVDK	240		
Db	176	VTVMWNSGSLSSVSHYTLQSALQGLYTMSSSVYVPSSTPMSQYVTCVSVAHPASSTYVDK	234		
Qy	241	RVEPKSCDKT--HTCP-----CPAPELLGSPVFLPPKPKDITLMTSRPEVYCVVDY	293		



Query Match	59.6%	Score 1498	DB 2	Length 470
Best Local Similarity	62.1%	Pred. No. 9, 6e-80		
Matches 292	Conservative	61	Mismatches 107	Indels 10
				Gaps 7
QY	8	LELVAILLGVOCCEVOLLTESSGGGLVDPGGLSLRLSCASCAGTFTSNYAMSWYRQAPKGLIENV	67	
DB	8	LEVLISAPICVLSQVQVLRSGPSPLVPRQGLSLITCVSGSSSLSSYALTWYRQAPKGALENV	67	
QY	68	SAISASGHSTYLAIDSVKGRFTISRDNKNITLYLQMNLSRAEPTAYAYYCAKDEVTMIYVL	127	
DB	68	GGIT-SSGOTTYINPMLKSLRSLITTKNSKSQVLSYSSVTEPTATYYCAR--TYEGEVG	123	
QY	128	NGGF-DYWGQGRYRVSSASTKGPENFLPAPSSKSTSGGTAALGCLVKDPPEPYATVSN	186	
DB	124	DGAIDAMGQGLLTVTSASSATPAKVYPLSSCCGDKSSSTVTLGCLVSSYMEPEYATVTNN	183	
QY	187	SGALTSQVHTPRPAVLQSSGLVSLSSVYVPPSSLTQYITCNVHNKFPSTKDKKVEPKS	246	
DB	184	SGALSGVHTPRPAVLQSSGLVSLSSMWTYVPGSTG-QFTCNVHNPASTSKDKKADP-T	241	
QY	247	CDKHTTCCPCPAPELLGGPSVFLPPKPKDTLMISTRPEVTCVYVDVSHEDDEVKFNWV	306	
DB	242	C-KRSPCCGCCPPPELPGPSVFLPPKPKDILTIGTPEVTCVYVDVGHDDDEVKFSWV	300	
QY	307	DGEVYHNAKTPREQYINSTRYVSLVLYLHODMLNGKEYKCKVSKNALPAPIETKISKA	366	
DB	301	DDVEYNTATTKPREQYINSTRYVSSALRIODHDMNGGKFKKYNHNEGIPAPIVTISRT	360	
QY	367	KGQRPPEQVYTLPPREMETKNQVSLTCLVCFKFPYSIDIAVEMESNQ--ENNNYKTTTPV	424	
DB	361	KGPAHEQVYTLAPQDELKSLVSLTCLMTVSFFDYDIAVEQRNQGPPSEDKYGTTPRQ	420	
QY	425	LDSGSEFLYLSKLYVDSKRMQGNVSCSVMEALHNHYTKSLSLSPGK	474	
DB	421	LDAOSSYLYLSKLYVDRNSWQEGDITVYVMEALHNHYTKSLSLSPGK	470	

```

RESULT 8
Ig gamma-2a chain - mouse
S37483
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision
C:Accession: S37483
R:Duncanell, F.F.D
Submitted to the EMBL Data Library, February 1993
A:Reference number: S37483
A:Accession: S37483
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-469 <DUC>
C:Cross-references: EMBL:X70423; NID:q406252; PIR:CAA9868.1; PID:q406253
C:Superfamily: Immunoglobulin C region; Immunoglobulin homology
C:Keywords: Immunoglobulin
F:276-345/Domain: immunoglobulin homology <IM>

Query Match          59.0%  Score 1482.5;  DB 2;  Length 469;
Best Local Similarity 59.0%;  Pred. No. 7,6e-79;
Matches 281;  Conservative 78;  Mismatches 104;  Indels 13;  Gaps 7

OY      4  GLSW-LRPLVILKVGCEVQLLESGGGLVQGGSLRLKSCAASGFTFSNYAMSWYRQAG 61
      ||| |||||  |||::||  ||::|||  ||::|||  ||::|||  ||::|||  ||::|||  ||
Db      2  GMSWIFELFLSTAGVHVGIOIQGSGPELVKRGAGVAKISCKASGVTFETDYLINWVKQKRG 61
      ||::|||  ||::|||  ||::|||  ||::|||  ||::|||  ||::|||  ||::|||  ||

OY      62  KGLEWVSAL-SASGHSITLADSVKRRFTISRDNKNITLYLQNSLRPAEDTAVYYCAKDR 120
      ||::|||  ||::|||  ||::|||  ||::|||  ||::|||  ||::|||  ||::|||  ||
Db      62  QGLKIGWGIYPASGNTKY-NENFKAKLTIVDTSSSTAYMQLSSITSEPTAVYFCARAMG 120
      ||::|||  ||::|||  ||::|||  ||::|||  ||::|||  ||::|||  ||::|||  ||

OY      121  VTMIVLNGEFGFYMGQGRVWYSSASTGSPVSEPLAPSPSKSSGGALGCLVKQFPEP 180
      |  ::  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      121  ATATLL-----DYMGQGITLTVSSAKTPASVYPLAPVCGDGTSSVTLGCLVKGTFPEP 175
      ||::|||  ||::|||  ||::|||  ||::|||  ||::|||  ||::|||  ||::|||  ||

OY      181  VTVSNAGALTVSGVHTPEAVLQSSGLSLSSVTVYTPSSSLGTQTYICNVNHRPSNTKYDK 240
      ||::|||  ||::|||  ||::|||  ||::|||  ||::|||  ||::|||  ||::|||  ||

```

Db	176	VTLINMGSSLSGVTTFPAVLQSD-LYTLSSSVYTVTSSWPQOSTICNVNHAASSTKVDK	234
QY	241	RVEPKSCDTHTCPP--CPAPELLGGPSVLEPPKPKDTLMTSTRPEVTCVVVDVSHEDP	298
Db	235	KIEPRG-PTIKRCPSPCKPAPRLTLGGPSFIEPRKIDWLISLSTIVCCVVVDSEDDP	293
QY	229	EVEFMWYVDGVEVNAHAKTKPREQVNSNYRNVSVYTLVHODMLNGEKYCKSNKLPAP	358
Db	294	DVQLSWFENNVNEVHTAQOTIHREDNSTLRYVSALEPIQIQMDMSGEFKCKVNNKDLPPAP	353
QY	359	IEKTSISKAKGPREQVYVTLPPRSREEMTKNQVSLTCLVKGFYPSDIAVMESNGPENNY	418
Db	354	IEERTISKPGSVARQPVVLPPEEEMTKKQVTLICMVTDFMPEIDYIVETVNGKTELNY	413
QY	419	KTPPVLVLDSDGSFLYSLKLTVDKSNQOGNVCVSMHEALNNHTQKLSLSPCK	474
Db	414	KNTPEVLDSDGSYFMYSKLRAEKKMVENNSYSCVHEGGLNNHTTKFSSTRPCK	469

[illegible]



F:251-320/Domain: immunoglobulin homology <IMM>  
F:22/Disulfide bonds: interchain (to 98) #status predicted  
F:99/Disulfide bonds: interchain (to 109) #status predicted

Query Match 60.8%; Score 1527.5; DB 2; Length 444;  
Best Local Similarity 61.4%; Pred. No. 1.8e-81;  
Matches 282; Conservative 71; Mismatches 87; Indels 19; Gaps 6;

QY EVQLLESGGGLVPGEGSLRLSCAASGFFPSNYAMSWVQAAPAKGLEWYSAIS--ASGHST 77  
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||  
DB 1 EVOXETGGGLVPRPNSLKLTLCTSGFTFSNVRHMLRPP3KRLEMTAVITVKSNDNGA 60  
  
QY YLADSVKGRFITSRDNSKNLTLYLOMNSLRARDTAYYCARKDREVTMIYVLNGGDYWGOG 137  
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||  
DB 61 KYAESVKRRFTISRDSKSSVYLQNNRLREEDTATYYCCRPWWY-----AMDGWGOG 113  
  
QY TRVTVYSASTGPSVFPLAPPSPSKSPSGGTALAGCLVKDYFEPEPVTSNMNGALTSGVHTF 197  
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||  
DB 114 TSVIYSSAKTTTPPSVYPIAPGSAQTNTSMVTLGCLVKGYFEPEPVTVTNSSLSGVHTF 173  
  
QY PAVLIQSGLYSLSSVYVPSSSLGTQYICNVNHKPSMTVDKRYEPAKCDKTKTHCP-- 255  
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||  
DB 174 PAVLIQSD-LYTLSSSYVPSSTWSEPTCVVAHPASSTKDKKIIVPRDC----CKPCI 228  
  
QY CPAPELLGSPVFLPPPKRKDTLMISRTPEYTCVVVDVSHDEPEKFKFWYDVGEVHNAAK 315  
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||  
DB 229 CTVEPV--SSVFTEPPPKPDVLTITLPKKYTCVAVDLSKIIDPEVQSFWDVDEVHTAQ 285  
  
QY TKPREEDYNSTRVAVSVYLVLDHODLNKEKCKVSNKNAFLAPIEKTSKAKGQPREPOV 375  
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||  
DB 286 TQPREEDQNSFRSVELPIIHODLNKEKCKRVNSAFLAPIEKTSKKGKRPKAQV 345  
  
QY YTLPPSRERMTKNOVSLTCLVKGFPSDIADVEMESNGOPEINIKYTPPVLDSDGSFELYS 435  
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||  
DB 346 YTIIPPKRQMAKDVSILTCMITDFPEDIFVEMOMNGPALNIKNTPQIMDDTSYFYVS 405  
  
QY KLTVDKSRMOOGANFVCSVMHEALHNHTOKSLSPCK 474  
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||  
DB 406 KLVNQKSNWEAGNFTCSVLHEGHHNHTKSLSHSPCK 444

RESULT 7  
S22080  
Ig heavy chain precursor (B/M/T.4A.17.H5.A5) - bovine  
N:Alternate names: Ig gamma-1 chain C region (clone 8.10)  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Jul-1999  
C:Accession: S22080; S06610; A31303  
R:Sanders, P.G.  
submitted to the EMBL Data Library, November 1991  
A:Reference number: S22080  
A:Accession: S22080  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-470 <SAN>  
A:Cross-references: EMBL:X62916; NID:g439; PIDN:CAA44639.1; PID:g4440  
R:Symons, D.B.A.; Clarkson, C.A.; Beale, D.  
Mol. Immunol. 26, 841-850, 1989  
A:Title: Structure of bovine immunoglobulin constant region heavy chain gamma 1 and g  
A:Reference number: S06610; MUID:90097956; PMID:2513487  
A:Accession: S06610  
A:Molecule type: DNA  
A:Residues: 142-470 <SYM>  
A:Cross-references: EMBL:X16701  
A>Note: The sequence was determined from the germline gene  
C:Genetics:  
A:Gene: Ig CH gamma-1  
A:Introns: 98/1; 111/1; 221/1  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: glycoprotein; heterotetramer; immunoglobulin; membrane protein  
F:161-225/Domain: immunoglobulin homology <IMM>  
F:318/Binding site: carbohydrate (Asn) (covalent) #status predicted

[illegible]





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 12, 2003, 12:57:09 ; Search time 35.4831 seconds  
(without alignments)  
1284.668 Million cell updates/sec

Title: US-09-848-832-3

Perfect score: 2514

Sequence: 1 MEFGLSWFLVAILKGVCE.....MHEALHNHYTKSLSPGK 474

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR\_76:\*  
2: PIR1:\*  
3: PIR2:\*  
4: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1758	69.9	330	1 GHU	Ig gamma-1 chain C
2	1639.5	65.2	377	2 A23511	Ig gamma-3 chain C
3	1637.5	65.1	377	2 A60764	Ig gamma-3 chain C
4	1610	64.0	326	1 G2HU	Ig gamma-2 chain C
5	1599.5	63.6	327	1 G4HU	Ig gamma-4 chain C
6	1527.5	60.8	444	2 PC4436	monoclonal antibody
7	1498	59.6	470	2 S22080	Ig heavy chain pre
8	1482.5	59.0	469	2 S37483	Ig gamma-2a chain
9	1455	57.9	472	2 S31459	Ig gamma-1 chain -
10	1442	57.4	374	2 S69339	Ig heavy chain V r
11	1429	56.8	446	2 S40295	Ig gamma-2a chain
12	1417	56.4	474	1 G2MS11	Ig gamma-2b chain
13	1401.5	55.7	475	2 S01321	Ig gamma-2b chain
14	1367	50.4	328	2 I47159	Ig gamma-2a chain
15	1361	50.2	328	2 I47160	Ig gamma-2b chain
16	1353	49.8	325	4 S31866	Ig gamma-1 chain C
17	1345	49.5	234	2 PT0207	Ig gamma chain C r
18	1335	49.1	328	2 I47158	Ig gamma-1 chain C
19	1231.5	49.0	323	1 GHRB	Ig gamma chain C r
20	1231	48.0	328	2 I47161	Ig gamma-3 chain C
21	1210.5	48.2	329	1 G2GP	Ig gamma-2 chain C
22	1165.5	46.4	308	2 C30554	Ig heavy chain C r
23	1157	46.0	289	1 G3HWI	Ig gamma-3 heavy C
24	1155	45.9	326	2 PS0017	Ig gamma-1 chain C
25	1150	45.7	329	1 G3MSC	Ig gamma-3 chain C
26	1145	45.5	324	1 G1MS	Ig gamma-1 chain C
27	1144.5	45.3	333	2 PS0018	Ig gamma-2b chain
28	1140	45.3	393	1 G1MSM	Ig gamma-1 chain C
29	1139	45.3	398	1 G3WSM	Ig gamma-3 chain C

30	1129	44.9	330	1 G2MSA	Ig gamma-2a chain
31	1127.5	44.8	329	2 S00847	Ig gamma-2c chain
32	1126.5	44.8	335	1 G2MSAB	Ig gamma-2a chain
33	1124	44.7	399	1 G2MSAM	Ig gamma-2a chain
34	1115	44.4	322	2 PS0019	Ig gamma-2a chain
35	1113	44.3	348	2 S38864	Ig epsilon chain C
36	1093.5	43.5	327	2 S06611	Ig gamma-2 chain C
37	1080	43.0	405	1 G2MSBM	Ig gamma-2 chain C
38	1070	42.6	277	2 I47162	Ig gamma-4 chain C
39	1003.5	39.9	249	2 S69340	Ig heavy chain VHI
40	879.5	35.0	572	2 B45529	Ig heavy chain (
41	868.5	34.5	549	2 S04845	Ig heavy chain pre
42	848	33.7	218	2 A36040	Ig heavy chain V-I
43	827	32.9	220	2 A49444	Ig gamma-1 heavy C
44	791.5	31.5	241	2 S69131	Ig heavy chain (D
45	791	31.5	627	2 S14683	Ig mu chain precu

#### ALIGNMENTS

##### RESULT 1

GHU

Ig gamma-1 chain C region - human

C:Species: Homo sapiens (man)

C:Date: 31-Jan-1981 #sequence\_revision 18-Aug-1982 #ext\_change 16-Jul-1999

C:Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146

R:Ellison, J.W.; Berson, B.J.; Hood, L.E.

Nucleic Acids Res. 10, 4071-4079, 1982

A:Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.

A:Reference number: A93433; MUID:82274238; PMID:6287432

A:Accession: A93433

A:Molecule type: DNA

A:Residues: 1-330 <BL>

A:Cross-references: EMBL:217370

A:Note: This sequence has the Gln(17) allelic marker, 97-Lys, and the Gln(1) marker

A:Note: Lys-330 is removed after translation

R:Harits, L.J.

submitted to the EMBL Data Library, October 1992

A:Reference number: S33904

A:Accession: S36861

A:Molecule type: DNA

A:Residues: 2-330 <HAR>

A:Cross-references: EMBL:217370

R:Rakhashli, N.; Ueda, S.; Obata, M.; Nakai, S.; Honjo, T.

Cell 29, 671-679, 1982

A:Title: Structure of human immunoglobulin gamma genes: implications for evolution of

A:Reference number: S33887; MUID:83001943; PMID:681139

A:Accession: S33887

A:Molecule type: DNA

A:Residues: 88-113;235-330 <TRK>

A:Cross-references: EMBL:217370

R:Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman

Biochemistry 9, 3161-3170, 1970

A:Title: The covalent structure of a human gammag-1 immunoglobulin. VII. Amino acid seq

A:Reference number: A90563; MUID:71064024; PMID:5489771

A:Contents: myeloma protein Eu

A:Accession: B90563

A:Molecule type: protein

A:Residues: 1-96,'R',98-135 <GUN>

A:Note: this sequence has the Gln(3) marker, 97-Arg

R:Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.

Biochemistry 9, 3171-3181, 1970

A:Title: The covalent structure of a human gammag-1 immunoglobulin. VIII. Amino acid se

A:Reference number: A90564; MUID:71064025; PMID:5530842

A:Contents: Eu

A:Accession: A90564

A:Molecule type: protein

A:Residues: 136-154,'Q',156-165,'Q',167-176,'Q',178-194,'N',196-197,'D',199-238,'E',2

A:Note: this sequence has the Gln(non-1) markers, 239-Glu and 241-Met

R:Ponstingl, H.; Hilschmann, N.  
Hope-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976  
A:Title: Die Primärstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein N)



```

Db      61  ERLEWVASISVCG-TTYYPDMSKGRFTISRDNANILYLQLSLSESDTAMVYCGCFAD 119
QY      121  VMIVIVLNGGFDMGCGTRATVSSASTKGPVFLPAPSSKSTSGTAAAGCLVKDYFPEP 180
Db      120  -----AMDYWGCGTLVTVSSASTKGPVFLPAPSSKSTSGTAAAGCLVKDYFPEP 170
QY      181  VTVSNMNGALTSVHFPPAVLOSGLYSLSSVVTVPSSSLGTQTYICNVNHRKSNTRKVDK 240
Db      171  VTVSNMNGALTSVHFPPAVLOSGLYSLSSVVTVPSSSLGTQTYICNVNHRKSNTRKVDK 230
QY      241  RVEPKSCDTHTCPCPAPBELLGSPVFLPPPKPKDTLMISRTPEVTCVVDVSHDEPEV 300
Db      231  RVEPKSCDTHTCPCPAPBELLGSPVFLPPPKPKDTLMISRTPEVTCVVDVSHDEPEV 290
QY      301  KFMWYDGYEVNNAKTRPEEOYNSTRVAVSVTLVHODMLNGEKYCKVSNKALPAPTE 360
Db      291  KFMWYDGYEVNNAKTRPEEOYNSTRVAVSVTLVHODMLNGEKYCKVSNKALPAPTE 350
QY      361  KTISKAKGQPREPQVYTLPPSRREEMTKNOVSLTCLVKGFPYPSDIAVEMESNGQPENNYKT 420
Db      351  KTISKAKGQPREPQVYTLPPSRREEMTKNOVSLTCLVKGFPYPSDIAVEMESNGQPENNYKT 410
QY      421  TTPVLDSDGSFPLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTOKSLSLSPGK 474
Db      411  TTPVLDSDGSFPLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTOKSLSLSPGK 464

RESULT 15
ABP58273
ID  ABP58273 standard; Protein; 449 AA.
XX
AC  ABP58273;
XX
DT  31-MAR-2003 (first entry)
XX
DE  Humanised 3D6 antibody heavy chain.
XX
KW  Monoclonal antibody; 3D6; complementarity determining region; CDR;
KW  mouse; human; humanised antibody; antibody; Alzheimer's disease;
KW  Down's syndrome; cerebral amyloid angiopathy; neuroprotective;
KW  nontoxic.
XX
OS  Chimeric - Mus sp.
OS  Chimeric - Homo sapiens.
XX
FH  Key
FH  Location/Qualifiers
FT  Region
FT  /note= "heavy chain variable region"
FT  Region
FT  /note= "CDR1"
FT  Region
FT  /note= "CDR2"
FT  Region
FT  /note= "CDR3"
FT  /note= "CDR3"
XX
PN  WO200288306-A2.
XX
PD  07-NOV-2002.
XX
PF  26-APR-2002; 2002WO-US11853.
XX
PR  30-APR-2001; 2001US-287539P.
XX
PA  (ELIL ) LILLY & CO ELI.
XX
PI  Tsurushita N, Vasquez M;
XX
DR  MPI; 2003-183835/18.
XX
PT  New humanized forms of mouse 3D6 antibodies, useful for treating Down's
PT  syndrome, (pre-)clinical Alzheimer's disease or (pre-)clinical cerebral
PT  amyloid angiopathy, or for inhibiting formation of or reducing Abeta

```

```

PT  plaque in the brain -
XX
PS  Claim 5; Page 10-11; 54pp; English.
CC  The present sequence is that of a preferred heavy chain of a
CC  humanised antibody of the present invention. In the variable region
CC  of this sequence, the complementarity determining regions (CDRs)
CC  originate from murine monoclonal antibody 3D6 and the framework region
CC  originates from human germline VH segment DP-45 and J segment JH4.
CC  Novel humanised antibodies of the invention have CDRs from 3D6 and
CC  human framework sequences. These humanised antibodies have binding
CC  affinities (affinity and epitope location) approximately the same
CC  as those of the mouse 3D6 antibody. The invention includes
CC  antibodies, single chain antibodies, and their fragments, as well
CC  as nucleotide sequences, vectors, transformed host cells, and
CC  methods of using the humanised antibody to treat, prevent,
CC  alleviate, reverse or otherwise ameliorate symptoms and/or
CC  pathology associated with Down's syndrome, (pre-)clinical
CC  Alzheimer's disease or (pre-)clinical cerebral amyloid angiopathy,
CC  and to inhibit formation or reduce Abeta plaque in the brain.
XX
SQ  Sequence 449 AA:
XX
Query Match 89.1%; Score 2241; DB 24; Length 449;
Best Local Similarity 92.3%; Pred. No. 3,7e-132;
Matches 420; Conservative 14; Mismatches 15; Indels 6; Gaps 1;

QY  20  EVQLVDSGGGLVQPGGSLRLSCAASGFTSNVAMSVRQAPGKGLEWVASIASGHTYL 79
Db  1  EVQLVDSGGGLVQPGGSLRLSCAASGFTSNVAMSVRQAPGKGLEWVASIRGGGRITYY 60
QY  80  ADSVKGRTISRDNKNTLYLQNSLRAEDTAYVYCAKREVMIVVLNGGFPDMGQGR 139
Db  61  SDNVKGRFTISRDNKNTLYLQNSLRAEDTAYVYVRRDH-----YGGSDYWGQGL 114
QY  140  VTVSSASTKGPVFLPAPSSKSTSGTAAAGCLVKDYFPEPYTVSNMNGALTSVHTFPA 199
Db  115  VTVSSASTKGPVFLPAPSSKSTSGTAAAGCLVKDYFPEPYTVSNMNGALTSVHTFPA 174
QY  200  VLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHRKSNTRKVDKREPKSCDTHTCPCPAP 259
Db  175  VLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHRKSNTRKVDKREPKSCDTHTCPCPAP 234
QY  260  ELGGPSVFLPPPKPKDTLMISRTPEVTCVVDVSHDEPEVKFMWYDGYEVNNAKTRP 319
Db  235  ELGGPSVFLPPPKPKDTLMISRTPEVTCVVDVSHDEPEVKFMWYDGYEVNNAKTRP 294
QY  320  EEOYNSTRVAVSVTLVHODMLNGEKYCKVSNKALPAPTEKTISKAKGQPREPQVYTL 379
Db  295  EEOYNSTRVAVSVTLVHODMLNGEKYCKVSNKALPAPTEKTISKAKGQPREPQVYTL 354
QY  380  PSREEMTKNOVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTTPPVLDSDGSFPLYSKLTV 439
Db  355  PSRDELTKNOVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTTPPVLDSDGSFPLYSKLTV 414
QY  440  DKSRLQGNVFCSCVMHEALHNHYTOKSLSLSPGK 474
Db  415  DKSRLQGNVFCSCVMHEALHNHYTOKSLSLSPGK 449

Search completed: September 12, 2003, 13:00:39
Job time : 83.0085 secs

```

XX New antibodies that interact with osteoprotegerin ligands, useful for  
PT treating osteoporotic disorders, e.g. osteoporosis, bone loss from  
PT arthritis, Paget's disease, osteopenia, osteomyelitis, hypercalcemia  
PT and osteonecrosis -  
XX  
XX Claim 1; Fig 2; 144pp; English.  
XX  
CC The invention relates to antibodies that interact with osteoprotegerin  
CC ligands (OPGL). The antibody is useful for detecting the level of OPGL in  
CC a biological sample. The antibody, or the pharmaceutical composition  
CC comprising the antibody, is also useful for treating osteoporotic disorder,  
CC an inflammatory condition with attendant bone loss, an autoimmune  
CC condition with attendant bone loss in a patient or rheumatoid arthritis  
CC in a patient. In particular, the antibody or composition is useful for  
CC treating bone diseases, e.g. osteoporosis, bone loss from arthritis,  
CC Paget's disease, osteopenia, endocrine osteoporosis (e.g. Cushing's  
CC syndrome or acromegaly), osteogenesis imperfecta, homocystinuria,  
CC Menkes' syndrome, Riley-Day syndrome, osteomyelitis, hypercalcemia, or  
CC osteonecrosis. The present sequence represents an anti-OPGL-1 antibody  
CC heavy chain.  
XX  
XX Sequence 467 AA:  
SQ  
Query Match 89.3%; Score 2244.5; DB 24; Length 467;  
Best Local Similarity 90.5%; Pred. No. 2.3e-132;  
Matches 429; Conservative 14; Mismatches 24; Indels 7; Gaps 3;  
QY 1 MEFGLSWFLVLAIKGVCEVOLLSEGGGLVDPGSLRLSCAASGFTFSNYAMSWVQAP 60  
DB 1 MEFGLSWFLVLAIKGVCEVOLLSEGGGLVDPGSLRLSCAASGFTFSNYAMSWVQAP 60  
QY 61 GKGLWWSAISASGSHSTYLDVSKGRFTISRDNKNTLYLQMSLRAEDTAVYYCAKDRE 120  
DB 61 GKGLWWSAISASGSHSTYLDVSKGRFTISRDNKNTLYLQMSLRAEDTAVYYCAKDRE 120  
QY 121 VTMLVNLNGGFYDYGQSTRTVSSASTKSPVFPPLAPSSKSGGTALCLVADYPERP 180  
DB 121 VTMLVNLNGGFYDYGQSTRTVSSASTKSPVFPPLAPSSKSGGTALCLVADYPERP 180  
QY 121 TTYIM--SWPDDMGQGTLYTVSSASATKSPVFPPLAPSSKSGGTALCLVADYPERP 177  
DB 121 TTYIM--SWPDDMGQGTLYTVSSASATKSPVFPPLAPSSKSGGTALCLVADYPERP 177  
QY 181 VTVSNMNGALTSQVHTPRVAVLQSSGLYSLSVTVTPSSISLGTQYTCNNVHKSNTYVDK 240  
DB 178 VTVSNMNGALTSQVHTPRVAVLQSSGLYSLSVTVTPSSISLGTQYTCNNVHKSNTYVDK 237  
QY 241 RVEKSCDKTHTCPPCAPPELLGLSPVFLPPPKKDTLMSRPPEVCYVVDVSHEDPEV 300  
DB 238 TVERKCCVE---CPPCAPR-VAGPSVFLPPPKKDTLMSRPPEVCYVVDVSHEDPEV 293  
QY 301 KFMWYDGVENVHNAKTRPREQYNSTYRVVSVLTVHLQDMLNKEKYCKVSNKALPAPIE 360  
DB 294 OFWNYDGVENVHNAKTRPREQYNSTYRVVSVLTVHLQDMLNKEKYCKVSNKALPAPIE 353  
QY 361 KITSKAKGPRERQVYTLPPSRREMTKNQVSLTCLVAGFTPSDIAVWESNGORENNYKT 420  
DB 354 KITSKTKGPRERQVYTLPPSRREMTKNQVSLTCLVAGFTPSDIAVWESNGORENNYKT 413  
QY 421 TPPLVLDGSEFFLYSKTLVDKSRMQGNVSCSYMHMLNNHYOKLSLSPGK 474  
DB 414 TPPLVLDGSEFFLYSKTLVDKSRMQGNVSCSYMHMLNNHYOKLSLSPGK 467

KW antithrombotic agent; myocardial infarction therapy.  
XX  
XX Synthetic.  
XX  
FH Key  
FT Peptide  
FT 13..19  
FT /label= Leader  
FT 20..134  
FT /label= VH  
FT 135..232  
FT /label= CH1  
FT 233..247  
FT /label= hinge  
FT 248..357  
FT /label= CH2  
FT 358..464  
FT /label= CH3  
FT Misc-difference  
FT /note= "translated stop codon"  
FT  
FT  
PN EP491351-A2.  
XX  
PD 24-JUN-1992.  
XX  
PF 17-DEC-1991; 91EP-0121591.  
XX  
PR 18-DEC-1990; 90JP-00413829.  
PR 11-NOV-1991; 91JP-0294464.  
XX  
PA (TAKE ) TAKEDA CHEM IND LTD.  
XX  
PI Iwasa S, Taka H, Watanabe T, Tada H;  
XX  
XX WPI. 1992-209528/26.  
DR N-PSDB; AAQ23692.  
XX  
PT Chimeric monoclonal antibodies - contain anti-human fibrin  
PT antibody light and heavy chain variable and constant for treating  
PT thrombotic conditions e.g. myocardial infarction  
XX  
PS Example; Figure 11; 87pp; English.  
XX  
XX  
CC plasmid pTB1373 contains the whole length of a mouse-human  
CC chimeric anti-human fibrin heavy chain cDNA open reading  
CC frame. It was prepd. using Poly(A)+ RNA from the anti-fibrin  
CC chimeric Ab-producing transformant FIB1-H01/X63 as a template  
CC to clone human C-kappa cDNA, using the oligo-dT (pharmacia) primer as  
CC a primer for first strand cDNA synthesis and the 5'C2H and 3'EH  
CC primers for the PCR. A human gamma-1 chain CH2-CH3 domain encoding  
CC cDNA was amplified. Similarly a human gamma-1 chain CH1 domain  
CC encoding cDNA and an anti-fibrin antibody VH cDNA and a leader  
CC peptide cDNA were amplified using the primers 3'EH, 3'C2H and 3'C1H  
CC respectively as a primer for first strand cDNA synthesis and the  
CC primer combination of 5'C1H and 3'C2H, of 5'EH and 3'C1H and of  
CC 5'EH and 3'EH respectively as primers for PCR. The amplified gene  
CC products were isolated and used to produce plasmids. After  
CC confirmation of the cDNA sequence of each plasmid, the cDNA  
CC encoding LH, VH, CH1 and CH2CH3 were joined together to give  
CC plasmid pTB1373 contg. the whole length chimeric H chain  
CC (LH, VH, CH1, CH2CH3), also abbreviated as IgH-F1H,  
CC (Updated on 25-MAR-2003 to correct PN field.)  
XX  
XX  
SQ Sequence 466 AA:  
Query Match 89.3%; Score 2244; DB 13; Length 466;  
Best Local Similarity 89.5%; Pred. No. 2.5e-132;  
Matches 424; Conservative 18; Mismatches 22; Indels 10; Gaps 2;  
QY 1 MEFGLSWFLVLAIKGVCEVOLLSEGGGLVDPGSLRLSCAASGFTFSNYAMSWVQAP 60  
DB 1 MDSRLNVLFLVLAIKGVCEVOLLSEGGGLVDPGSLRLSCAASGFTFSNYAMSWVQAP 60  
QY 61 GKGLWWSAISASGSHSTYLDVSKGRFTISRDNKNTLYLQMSLRAEDTAVYYCAKDRE 120



AAE33522  
 ID AAE33522 standard; Protein; 447 AA.  
 XX  
 AC AAE33522;  
 XX  
 DT 02-APR-2003 (first entry)  
 XX  
 XX Human AQC2 heavy chain protein.  
 DE  
 XX Human; very late activation antigen: VLA-1; beta1 containing integrin;  
 KM immunological disorder; inflammatory disorder; skin related condition;  
 KM psoriasis; eczema; burn; dermatitis; respiratory distress syndrome;  
 KM fibrosis; allergic rhinitis; asthma; bronchitis; tendonitis; bursitis;  
 KM fever; migraine headache; inflammatory bowel disease; Crohn's disease;  
 KM irritable bowel syndrome; colitis; colorectal cancer; vascular disease;  
 KM atherosclerosis; thyroiditis; aplastic anaemia; periarthritis nodosa;  
 KM gastritis; Hodgkin's disease; rheumatic fever; autoimmune disease;  
 KM osteoarthritis; type I diabetes; myasthenia gravis; rheumatoid arthritis;  
 KM systemic lupus erythematosus; multiple sclerosis; nephrotic syndrome;  
 KM renal failure; sarcoidosis; Behcet's syndrome; gingivitis; polymyositis;  
 KM hypersensitivity; graft rejection; transplant rejection; conjunctivitis;  
 KM graft versus host disease; myocardial ischaemia.  
 XX  
 XX Homo sapiens.  
 OS  
 XX WO200283854-A2.  
 PN  
 XX 24-OCT-2002.  
 PD  
 XX 12-APR-2002; 2002WO-US11521.  
 PF  
 XX 13-APR-2001; 2001US-283794P.  
 PR  
 XX 06-JUL-2001; 2001US-303689P.  
 XX  
 XX (BIOI ) BIOGEN INC.  
 PA  
 XX Lyne PD, Garber EA, Saldanha JW, Karpusas M;  
 PI  
 XX WPI: 2003-093009/08.  
 DR  
 XX  
 XX New anti-VLA-1 antibodies are useful for preventing or treating  
 PT VLA-1-mediated immunological or inflammatory disorders, e.g. psoriasis,  
 PT eczema, burns, dermatitis, and abnormal proliferation of hair follicle  
 PT cells or fibrosis -  
 PT  
 XX  
 PS Claim 6; Page 75; 248pp; English.  
 CC The present invention relates to novel antibodies that specifically bind  
 CC to very late activation (VLA-1; beta1 containing integrins) antigens and  
 CC methods of using these antibodies to treat immunological disorders. The  
 CC anti-VLA-1 antibodies are useful for preventing or treating VLA-1-  
 CC mediated immunological or inflammatory disorders such as skin related  
 CC conditions (e.g. psoriasis, eczema, burns, dermatitis and abnormal  
 CC proliferation of hair follicle cells), fibrosis (e.g. kidney or lung  
 CC fibrosis), allergic rhinitis, respiratory distress syndrome, asthma,  
 CC bronchitis, tendonitis, bursitis, fever, migraine headaches, gastro-  
 CC intestinal conditions (e.g. inflammatory bowel disease, Crohn's disease,  
 CC gastritis, irritable bowel syndrome, colitis and colorectal cancer),  
 CC vascular diseases (e.g. atherosclerosis), thyroiditis, aplastic anaemia,  
 CC periarthritis nodosa, Hodgkin's disease, rheumatic fever, osteoarthritis,  
 CC autoimmune diseases (e.g. type I diabetes, myasthenia gravis, rheumatoid  
 CC arthritis, systemic lupus erythematosus and multiple sclerosis), renal  
 CC failure, sarcoidosis, nephrotic syndrome, Behcet's syndrome, gingivitis,  
 CC polymyositis, hypersensitivity (e.g. delayed type hypersensitivity or  
 CC immediate hypersensitivity), graft and transplant rejections, graft  
 CC versus host disease, conjunctivitis, swelling occurring after injury,  
 CC myocardial ischaemia or endotoxin shock syndrome. The present sequence  
 CC is human AQC2 heavy chain protein.  
 CC  
 XX  
 SQ Sequence 447 AA;

Query Match 89.3%; Score 2244.5; DB 24; Length 447;  
 Best Local Similarity 93.2%; Pred. No. 2.2e-132;

Matches 426; Conservative 6; Mismatches 12; Indels 13; Gaps 3;  
 QY 20 EVQLVESGGGLVQPGGSLRLSCAASGFTSSNAMSVRQAPGKGLVWSAIGASHSTYL 79  
 DB 1 EVQLVESGGGLVQPGGSLRLSCAASGFTSSRYTMSVRQAPGKGLVWSAIGASHSTYL 59  
 QY 80 ADSVKGRTISRDNSKNTLYLQMNSLRADDTAVYCCAK--DREVTMIIVLNGGFDYMGQ 136  
 DB 60 LDSVKGRTISRDNSKNTLYLQMNSLRADDTAVYCTRGFGD-----GGYEDYMGQ 110  
 QY 137 GTRVYSSASTKGPVSFPLAPSSKSTSGTAAAGCLVMDYFPEPVTVSNNGALVSGVHT 196  
 DB 111 GRLVTVSSASTKGPVSFPLAPSSKSTSGTAAAGCLVMDYFPEPVTVSNNGALVSGVHT 170  
 QY 197 FRAVYQSSGLYSLSSVYTPYSSSLGTQITICVNNHKSPTKDKRREPSCDKTHTCPQC 256  
 DB 171 FRAVYQSSGLYSLSSVYTPYSSSLGTQITICVNNHKSPTKDKRREPSCDKTHTCPQC 230  
 QY 257 PAPELLGSPVFPPPKPDTLMISRTPEVTCVVVDVSHEDPEVKFNNYVDDGEVHNMAKT 316  
 DB 231 PAPELLGSPVFPPPKPDTLMISRTPEVTCVVVDVSHEDPEVKFNNYVDDGEVHNMAKT 290  
 QY 317 KPREQYNSTYRVYSVLVVLIHQAQMNGKERKCKVSNKALPAPIEKTISSAKGQPREPPQVY 376  
 DB 291 KPREQYNSTYRVYSVLVVLIHQAQMNGKERKCKVSNKALPAPIEKTISSAKGQPREPPQVY 350  
 QY 377 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEESNQGPENNYKTPPVLDGSGFFLYSK 436  
 DB 351 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEESNQGPENNYKTPPVLDGSGFFLYSK 410  
 QY 437 LTVDKSRMQQGNVFCSCVMHEALHNHYTQKSLSLSPG 473  
 DB 411 LTVDKSRMQQGNVFCSCVMHEALHNHYTQKSLSLSPG 447

RESULT 13  
 ID ABP71365  
 ABP71365 standard; Protein; 467 AA.  
 XX  
 AC ABP71365;  
 XX  
 DT 28-APR-2003 (first entry)  
 XX  
 DE Anti-OPGL-1 antibody heavy chain.  
 XX  
 XX Osteoprotegerin ligand; osteopathic; antinflammatory; antirheumatic;  
 KW antirheumatic; cytoskeletal; OPGL; anti-OPGL-1; antibody.  
 KW  
 OS Mus musculus.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..19 /note= "Irg2 signal peptide"  
 FT Region 20..141 /note= "variable region"  
 FT Region 142..467 /note= "constant region"  
 FT  
 PN WO2003002713-A2.  
 PD 09-JAN-2003.  
 XX  
 PD 25-JUN-2002; 2002WO-US20181.  
 PF 26-JUN-2001; 2001US-301172P.  
 PR  
 PA (ABGE-) ABGENIX INC.  
 PA (AMGE-) AMGEN INC.  
 XX  
 XX Boyle WJ, Martin FH, Corvalan JR, Davis GC;  
 PI  
 XX WPI: 2003-210262/20.  
 DR N-PSDB; AB859147.

XX New chimeric T84.12 antibody active against carcinoembryonic  
PT antigen - has murine variable and human constant regions, also  
PT DNA encoding it and transformed myeloma cells  
XX  
PS Claim 1: Page 22-23; 27pp; English.  
XX  
CC The sequences (AA054651-52) show the light and heavy chain CDNA  
CC of murine T84.12. The T84.12 antibody is directed against the  
CC tumour marker carcinoma embryonic antigen, and is useful for  
CC tumour imaging and immunotherapy.  
CC The amino acid sequence given in the specification has been  
CC incorrectly identified as a nucleic acid sequence, therefore  
CC unacceptable characters have been represented as an 'N'.  
CC The amino acid sequence given below has been derived from the  
CC cDNA, by the indexer.  
CC (Updated on 25-MAR-2003 to correct PN field.)  
XX  
XX Sequence 477 AA:  
SO  
Query Match 89.8%; Score 2257; DB 15; Length 477;  
Best Local Similarity 89.2%; Pred. No. 3.9e-133;  
Matches 423; Conservative 23; Mismatches 22; Indels 6; Gaps 2;  
QY 1 MEGLSLWLFVLAIIKGVQCEVQLLESGGLVOPGSLRLSCAASGFTFSNYAMSWVQAP 60  
DB 10 MNFGSLFLFLVYLKGVQCEVQLLESGGLVOPGSLRLSCAASGFTFSNYAMSWVQAP 69  
QY 61 GKGLEWYSAISAGSHRYLADSVKGRFTISRDNSKNTLYLQMNSLRADTVAYYCAKRE 120  
DB 70 EKRLIEWASISSDG-TFFYVDVSKGRFTVSRDANKRLIYLQMSLSRSDTAMYYCAR--- 125  
QY 121 VTMIIVLNGGFDYMGQTRVTVSSASTKGPVFPFLAPSSKTSGGTALGCLVNDYFPEP 180  
DB 126 --IDYGGGGGYGQGLTAVSAASTKGPVFPFLAPSSKTSGGTALGCLVNDYFPEP 183  
QY 181 VTVSMNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHRKPSNTKYDK 240  
DB 184 VTVSMNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHRKPSNTKYDK 243  
QY 241 RVEKSCDKHTPCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDASHEDEV 300  
DB 244 KVEKSCDKHTPCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDASHEDEV 303  
QY 301 KFNMYVDGVEVHNNAKTRPREQYNSTYRVSVLTFLVHODMLNGEKYCKVSNKALPAPIE 360  
DB 304 KFNMYVDGVEVHNNAKTRPREQYNSTYRVSVLTFLVHODMLNGEKYCKVSNKALPAPIE 363  
QY 361 KTISKAKGQPREPQVYTLPPSRDEMTKNQVSLTCLVKGFPYSDIAVEMESNGOPENNYKT 420  
DB 364 KTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFPYSDIAVEMESNGOPENNYKT 423  
QY 421 TTPVLDSGGSFFLYSKLTVDKSRMQGQNVFSCSVMEHALHNHYTOKSLSLSPGK 474  
DB 424 TTPVLDSGGSFFLYSKLTVDKSRMQGQNVFSCSVMEHALHNHYTOKSLSLSPGK 477  
RESULT 11  
AAE34876  
ID AAE34876 standard; Protein: 444 AA.  
XX  
XX AAE34876;  
XX  
XX 28-MAY-2003 (first entry)  
XX  
XX B1WA4/8 antibody heavy chain mature protein.  
XX  
XX B1WA8 antibody; heavy chain variable region; light chain variable region;  
XX VH; VL; CD44v6; medicament; cancer; antibody therapy.  
XX  
XX Unidentified.  
XX  
XX WO200294879-A1.

XX  
PD 28-NOV-2002.  
XX  
XX 17-MAY-2002; 2002WO-EP05467.  
XX  
XX 18-MAY-2001; 2001EP-0112237.  
XX  
XX 26-SEP-2001; 2001US-325147P.  
XX  
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.  
XX (BOEH) BOEHRINGER INGELHEIM PHARM INC.  
XX  
PI Adolf G, Ostermann E, Patzelt E, Spiroli M, Heijer K, Miglietta JU;  
PI Van Dongen AAMS;  
XX  
XX WPI; 2003-129413/12.  
DR N-PSDB; AAD53212, AAD53215.  
XX  
XX New antibodies specific for an epitope coded by the variant exon of the  
PT CD44 gene, useful for treating cancer, including non-small cell lung,  
PT breast, head and neck, ovarian and lung cancer  
XX  
PS Claim 24; Column 44; 78pp; English.  
XX  
XX The present invention relates to novel antibody molecules comprising a  
CC variable region of the heavy (VH) and/or light chain (VL) of CD44v6  
CC specific humanised antibody called B1WA8 and B1WA4. Sequences of the  
CC invention are useful for manufacturing a medicament and for treating  
CC cancer including colorectum, non-small cell lung, breast, head and neck,  
CC ovarian, lung, bladder, pancreatic cancer or metastatic cancers of the  
CC brain. They are also useful in antibody therapy. The present sequence  
CC is B1WA4/8 antibody heavy chain mature protein. This sequence is used  
CC in the exemplification of the invention.  
XX  
XX Sequence 444 AA:  
SO  
Query Match 89.5%; Score 2249.5; DB 24; Length 444;  
Best Local Similarity 92.7%; Pred. No. 1.1e-132;  
Matches 422; Conservative 12; Mismatches 10; Indels 11; Gaps 1;  
QY 20 EVOLLESGGLVOPGSLRLSCAASGFTFSNYAMSWVQQAQKGLIEWYSAISAGSHRYL 79  
DB 1 EVOLLESGGLVOPGSLRLSCAASGFTFSNYAMSWVQQAQKGLIEWYSAISAGSHRYL 60  
QY 80 ADSVKGRTISRDNKNTLYLQMNSLRADTVAYYCAKDRZYVTMIIVLNGGFDYMGQTR 139  
DB 61 LDSIKGRTISRDNKNTLYLQMNSLRADTVAYYCAQ-----GLDWGRGRTL 109  
QY 140 VTVSSASTKGPVFPFLAPSSKTSGGTALGCLVNDYFPEPVTVSMNSGALTSGVHTFPA 199  
DB 110 VTVSSASTKGPVFPFLAPSSKTSGGTALGCLVNDYFPEPVTVSMNSGALTSGVHTFPA 169  
QY 200 VLOSSGLYSLSSVTVTPSSSLGTQTYICNVNHRKPSNTKYDKRVERKSCDKHTPCPCAP 259  
DB 170 VLOSSGLYSLSSVTVTPSSSLGTQTYICNVNHRKPSNTKYDKRVERKSCDKHTPCPCAP 229  
QY 260 ELIGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEKFNMYVDGVEVHNNAKTRPR 319  
DB 230 ELIGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEKFNMYVDGVEVHNNAKTRPR 289  
QY 290 EEQYNSTYRVSVLTFLVHODMLNGEKYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 349  
DB 320 EEQYNSTYRVSVLTFLVHODMLNGEKYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 379  
QY 380 PSREEMTKNQVSLTCLVKGFPYSDIAVEMESNGOPENNYKTTPVLDSGGSFFLYSKLTV 439  
DB 350 PSREEMTKNQVSLTCLVKGFPYSDIAVEMESNGOPENNYKTTPVLDSGGSFFLYSKLTV 409  
QY 440 DKSRMQGQNVFSCSVMEHALHNHYTOKSLSLSPGK 474  
DB 410 DKSRMQGQNVFSCSVMEHALHNHYTOKSLSLSPGK 444  
RESULT 12

```

Cc      113  OGTLYVSSASTKGPVFLAPSSKSTSGTALGCLVKDYFPEPTVSNNSGALTSGVH 172
Qy      196  TFPAYVQSSGLYSLSSVTVTPSSSLGTQYITICVNNHKRPSTKYDKRVEPKSCQKTHRCPP 255
Db      173  TFPAYVQSSGLYSLSSVTVTPSSSLGTQYITICVNNHKRPSTKYDKRVEPKSCQKTHRCPP 232
Qy      256  CPAPELLGSPSVFLFPKPKDPTLMISRTPEVTCVVDVSHEDPEVKFNMYVDGEVHNAK 315
Db      233  CPAPELLGSPSVFLFPKPKDPTLMISRTPEVTCVVDVSHEDPEVKFNMYVDGEVHNAK 292
Qy      316  TKPREQYNSTYRVSVLVTLVHODWLNKGEYKCKVSKNALPADIETISKAKQPREPOV 375
Db      293  TKPREQYNSTYRVSVLVTLVHODWLNKGEYKCKVSKNALPADIETISKAKQPREPOV 352
Qy      376  YTLPSREEMTKNOVSLTCLVKGFYPSDIAVEWESNGQPRNNKTPPVLDSDGSFPLYs 435
Db      353  YTLPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPRNNKTPPVLDSDGSFPLYs 412
Qy      436  KLTVDKSRMOQGNVFCSCVMHEALHNHYTOKSLSLSPGK 474
Db      413  KLTVDKSRMOQGNVFCSCVMHEALHNHYTOKSLSLSPGK 451

RESULT 9
ABUS8807
ID  ABUS8807 standard; Protein; 451 AA.
XX
AC  ABUS8807;
XX
DT  15-APR-2003 (first entry)
XX
DE  Mucin 1 (MUC-1) binding immunoglobulin kappa heavy chain.
XX
KW  Mucin-1-specific binding member; human; cancer; adenocarcinoma;
KW  breast cancer; ovarian cancer; bladder cancer; lung cancer;
KW  anti-cancer regimen; anti-cancer drug; radiation treatment.
XX
OS  Homo sapiens.
XX
PN  US2002146750-A1.
XX
PD  10-OCT-2002.
XX
PF  30-MAR-2001; 2001US-082698.
XX
PR  30-MAR-2000; 2000US-0538913.
XX
PA  (HOOG/) HOOGENBOOM H R J M.
XX
PA  (HEND/) HENDERIKX M P G.
XX
PI  Hoogenboom HRJM, Henderikx MPG;
XX
DR  MPI; 2003-198057/19.
XX
DR  N-PSDB; ABX79100.
XX
PT  Isolated mucin-1-specific binding member for diagnosing and/or treating
PT  cancer, e.g. breast cancer, comprises antigen binding domain having
PT  region that contains specific amino acid sequence -
XX
PS  Claim 12; Page 41-42; 70pp; English.
XX
XX  The invention describes an isolated mucin-1-specific binding member
Cc  having an antigen binding domain including a region that comprises a
Cc  specific amino acid sequence. The inventive MUC1-specific binding member
Cc  is used in the diagnosis and/or treatment of cancer, e.g. adenocarcinoma,
Cc  found in various tissues, e.g. breast, ovary, bladder, and lung. It
Cc  can be used alone or as a component in a more complex anti-cancer regimen
Cc  which may contain anti-cancer drug(s) and/or radiation treatment(s).
Cc  The inventive binding member recognizes tumour-associated MUC1 on
Cc  adenocarcinoma. Its affinity is high enough to bind to tumour cells.
Cc  This is the amino acid sequence of a mucin 1 (MUC-1) specific antibody
Cc  region used to isolate MUC-1 antigen binding domains for use in the

```

```

Cc      20  ENQLLESGLVNGPGSLRISCAASGTFEINMAMSWROAPGGLLEVSAISAGSTYL 79
Qy      1  QVQLVDSGGGLVPGGSLRLISCAASGTFEINMAMGWROAPGGLLEVSGISGSGSTYI 60
Db      80  ADSVKGHFTISRNSKNTLYLQNSLRAEDTAVYYCAKADREYTMIVLNGG---FDYWG 135
Qy      61  ADSVKGHFTISRNSKNTLYLQNSLRAEDTAVYYCAK-----TGGGVMDPIDYWG 112
Db      136  QGTRVTVSSASTKGPVFLAPSSKSTSGTALGCLVKDYFPEPTVSNNSGALTSGVH 195
Qy      113  OGTLYVSSASTKGPVFLAPSSKSTSGTALGCLVKDYFPEPTVSNNSGALTSGVH 172
Db      196  TFPAYVQSSGLYSLSSVTVTPSSSLGTQYITICVNNHKRPSTKYDKRVEPKSCQKTHRCPP 255
Qy      173  TFPAYVQSSGLYSLSSVTVTPSSSLGTQYITICVNNHKRPSTKYDKRVEPKSCQKTHRCPP 232
Db      256  CPAPELLGSPSVFLFPKPKDPTLMISRTPEVTCVVDVSHEDPEVKFNMYVDGEVHNAK 315
Qy      233  CPAPELLGSPSVFLFPKPKDPTLMISRTPEVTCVVDVSHEDPEVKFNMYVDGEVHNAK 292
Db      316  TKPREQYNSTYRVSVLVTLVHODWLNKGEYKCKVSKNALPADIETISKAKQPREPOV 375
Qy      293  TKPREQYNSTYRVSVLVTLVHODWLNKGEYKCKVSKNALPADIETISKAKQPREPOV 352
Db      376  YTLPSREEMTKNOVSLTCLVKGFYPSDIAVEWESNGQPRNNKTPPVLDSDGSFPLYs 435
Qy      353  YTLPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPRNNKTPPVLDSDGSFPLYs 412
Qy      436  KLTVDKSRMOQGNVFCSCVMHEALHNHYTOKSLSLSPGK 474
Db      413  KLTVDKSRMOQGNVFCSCVMHEALHNHYTOKSLSLSPGK 451

RESULT 10
AAR47453
ID  AAR47453 standard; Protein; 477 AA.
XX
AC  AAR47453;
XX
DT  25-MAR-2003 (updated)
DT  24-JUN-1994 (first entry)
XX
DE  chIT84.12 H3 heavy chain.
XX
KW  Chimeric; carcinoembryonic antigen; CCA; murine; mouse; constant;
KW  region; transform; myeloma cell; light chain; tumour.
XX
OS  Synthetic.
XX
PN  WO9325237-A1.
XX
PD  23-DEC-1993.
XX
PF  15-JUN-1993; 93MO-US05709.
XX
PR  15-JUN-1992; 92US-0904074.
XX
PA  (CITY ) CITY OF HOPE.
PA  (YANG/) YANG Y.
XX
PI  Fischer R, Paxton R, Shively JE, Wu A, Yang YHJ;
XX
XX  Yang YH;
XX
DR  MPI; 1994-007204/01.
DR  N-PSDB; AAO54655.

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PN WO20028306-A2.  
 XX 07-NOV-2002.  
 PD  
 XX  
 XX 26-APR-2002; 2002MO-US11853.  
 PF  
 XX 30-APR-2001; 2001US-287539P.  
 PR  
 XX (ELIL ) LILLY & CO ELI.  
 PA  
 XX Tsurushita N, Vasquez M;  
 PI  
 XX  
 XX  
 DR N-PSDB; AB224633, AB224635.  
 DR  
 XX  
 XX  
 PT New humanized forms of mouse 3D6 antibodies, useful for treating Down's  
 PT syndrome, (pre-)clinical Alzheimer's disease or (pre-)clinical cerebral  
 PT amyloid angiopathy, or for inhibiting formation of or reducing Abeta  
 PT plaque in the brain -  
 XX  
 XX  
 PS Disclosure; Page 13-14; 54pp; English.  
 CC The present sequence is that of a preferred heavy chain of a  
 CC humanised antibody of the present invention. In the variable  
 CC region of this sequence, the complementarity determining regions  
 CC (CDRs) originate from murine monoclonal antibody 3D6 and the  
 CC framework region from human germline VH segment DP-45 and J segment  
 CC JH4. Novel humanised antibodies of the invention have CDRs from 3D6  
 CC and human framework sequences. These humanised antibodies have  
 CC binding affinities (affinity and epitope location) approximately the  
 CC same as those of the mouse 3D6 antibody. The invention includes the  
 CC antibodies, single chain antibodies, and their fragments, as well  
 CC as nucleotide sequences, vectors, transformed host cells, and  
 CC methods of using the humanised antibody to treat, prevent,  
 CC alleviate, reverse or otherwise ameliorate symptoms and/or  
 CC pathology associated with Down's syndrome, (pre-)clinical  
 CC Alzheimer's disease or (pre-)clinical cerebral amyloid angiopathy,  
 CC and to inhibit formation or reduce Abeta plaque in the brain.  
 CC  
 XX  
 XX  
 SQ Sequence 468 AA:  
 Query Match 92.1%; Score 2315; DB 24; Length 468;  
 Best Local Similarity 91.6%; Pred. No. 9.1e-137;  
 Matches 434; Conservative 16; Mismatches 18; Indels 6; Gaps 1;  
 QY 1 MEGGLSWLFLVALKQCEVQLLESGGGLVQPGSGRLSCAASGFTFSNYAMSWAQAP 60  
 DB 1 MNGFLSLIFLVLVKQCEVOLVESGGGLVQPGSGRLSLSCAGSFPSNYGMSWROAP 60  
 QY 61 GKGLVWVSATISAGSHSTYLADSVKGRFTISRDNKMTLYQMNSLRAEDPAVYYCAKRE 120  
 DB 61 GKGLVWVSATISAGSHSTYLADSVKGRFTISRDNKMTLYQMNSLRAEDPAVYYCAKRE 120  
 QY 121 VTMIIVLVNGGEFDYWGCGTRVTVSSASTKGPVPLAPSSKSTSGTAAALCLVKYDPEP 180  
 DB 121 -----YSGGSDYWGCGTLVTVSSASTKGPVPLAPSSKSTSGTAAALCLVKYDPEP 174  
 QY 181 VTVSMNSGALTSGVHFRPAVLQSSGLYSLSVYTVPSSTLGTQTYICNNVHKSNKRYDK 240  
 DB 175 VTVSMNSGALTSGVHFRPAVLQSSGLYSLSVYTVPSSTLGTQTYICNNVHKSNKRYDK 234  
 QY 241 RVEPKSCDKTHTPCPCPAPRLGLGSPSYFLRPPKPKDTLMISRTPEVYCVAVVDSHEDPEV 300  
 DB 235 KVEPKSGDKTKHTPCPCPAPRLGLGSPSYFLRPPKPKDTLMISRTPEVYCVAVVDSHEDPEV 294  
 QY 301 KFMWYVDGVEVNAKTKPREBOYNSTYRVVSVLTVLHDMVLNCKEYCKVSNKALPAPIE 360  
 DB 295 KFMWYVDGVEVNAKTKPREBOYNSTYRVVSVLTVLHDMVLNCKEYCKVSNKALPAPIE 354  
 QY 361 KITSKAKGQREPOVYTLTPRSREEMTKNOVSLTCLVKGFPSPDIIVEMESNGPENNYKT 420  
 DB 355 KITSKAKGQREPOVYTLTPRSREEMTKNOVSLTCLVKGFPSPDIIVEMESNGPENNYKT 414

QY 421 TPVYLDSDGSFFLYSKLVVDKSRWQGNVFSQSVYMEHALNH YTKSLSPCK 474  
 DB 415 TPVYLDSDGSFFLYSKLVVDKSRWQGNVFSQSVYMEHALNH YTKSLSPCK 468  
 RESULT 5  
 AAR20057  
 ID AAR20057 standard; Protein: 475 AA.  
 XX  
 AC AAR20057;  
 XX  
 DT 25-MAR-1992 (first entry)  
 DT  
 XX  
 DE Heavy chain of 3D6 anti-HIV antibody.  
 XX  
 KW Plasmid pUC3D6HC; human immunodeficiency virus; AIDS;  
 KM complementarity determining region.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..19  
 FT /label= signal  
 FT Region 20..49  
 FT /label= Framework\_1  
 FT Region 50..54  
 FT /label= CDR-1  
 FT Region 55..68  
 FT /label= Framework\_2  
 FT Region 69..85  
 FT /label= CDR\_2  
 FT Region 86..117  
 FT /label= Framework\_3  
 FT Region 118..134  
 FT /label= CDR\_3  
 FT Region 135..145  
 FT /label= Framework\_4  
 FT Region 146..475  
 FT /label= Constant\_region  
 XX  
 PN WO9118983-A.  
 XX  
 PD 12-DEC-1991.  
 XX  
 PF 28-MAY-1991; 91WO-1000067.  
 XX  
 PR 29-MAY-1990; 90AT-0001178.  
 XX  
 PA (JUNG/) JUNGBAUER A.  
 XX  
 PI Felgenhauer M, Himmeler G, Kohl J, Steindl F;  
 DR N-PSDB; AAQ20066.  
 DR  
 PT Recombinant protein which binds to complex viral antigen and  
 PT HIV-1 - contains variable region of antibody derived from 3D6  
 PT cell line, used for detecting HIV-1 antigen  
 XX  
 PS Claim 2; Page 24; 52pp; German.  
 XX  
 CC The variable region of the heavy chain is used in a recombinant  
 CC protein with the variable region from the kappa light chain of 3D6,  
 CC the two V regions being joined by a linker. The recombinant protein  
 CC binds to HIV gp160.  
 CC See also AAQ20067 and AAQ20068.  
 XX  
 SQ Sequence 475 AA:  
 Query Match 91.9%; Score 2309.5; DB 13; Length 475;  
 Best Local Similarity 91.4%; Pred. No. 2e-136;  
 Matches 438; Conservative 13; Mismatches 19; Indels 9; Gaps 2;

0y	421	TPPVLDSDGSFFLYSKLTVDKSRWQQGNFSCSVMEALHNHYTQKSLSLSPGK	474
Db	421	TPPVLDSDGSFFLYSKLTVDKSRWQQGNFSCSVMEALHNHYTQKSLSLSPGK	474

```

RESULT 3
AAU14288
ID AAU14288 standard; Protein; 477 AA

```

AC AAU14288;

DT 24-OCT-2001 (first entry)

DE Human novel protein #159.

KM Human; novel protein; Antianaemic; osteopathic; antiinflammatory;  
KM Immunomodulatory; cytosolic; neuroprotective; vulnere; neutrophil;  
KM anticonvulsant; antiallergic; cerebroprotective; antifungal; antiviral;  
KM antimicrobial; antiallergic; dermatological; hemostatic; antistatic;  
KM thrombolytic; immunogen; antibody; gene therapy; neurological disorder;  
KM Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis  
KM tissue regeneration; immune disorder

OS Homo sapiens.

PN WO200155437-A2

PD 02-AUG-2001.

PF 25-JAN-2001; 2001WO-US02623

PR 25-JAN-2000; 2000US-0491404.

PA (HYSE-) HYSEQ INC.

PI Tang YT, Llu C, Drmanac RT;

DR WPT; 2001-451939/48.

DR N-PSDB; AAS22593.

PT Isolated polypeptides useful for treating anti-inflammatory diseases, nervous system disorders, and for regenerating bone and cartilage -

PS Example 4; Page 611-612; 894pp; English.

CC The invention relates to polynucleotides encoding novel human  
CC proteins or their active domains. The polypeptides, polynucleotides and  
CC antibodies raised against the polypeptides are used in a method of  
CC treatment of a mammal and prevention of disorders caused by the aberrant  
CC protein expression or activity. The polypeptides can be used as  
CC molecular weight markers, food supplements, and in antibody production.  
CC The polypeptides are used to identify compounds which bind to the  
CC polypeptides. Polynucleotides of the invention are used as probes and  
CC primers, for sequencing, for chromosome or gene mapping, in the  
CC production of recombinant proteins, and in generating anti-sense DNA or  
CC RNA and in gene therapy. Polypeptides of the invention can be used to  
CC target drugs to a tumour, in assays to determine biological activity, to  
CC raise antibodies/elicit an immune response, to determine quantitative  
CC protein levels, as tissue markers, and to isolate receptors or ligands.  
CC Polypeptides of the invention may also be useful in treating platelet  
CC disorders, stem cell disorders, regenerating bone, cartilage, tendon,  
CC ligament and/or nerve tissue, wound healing, treating burns, promoting  
CC the proliferation, differentiation and survival of stem cells, as a  
CC contractile, treating osteoporosis and osteoarthritis, anaemia,  
CC Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral  
CC sclerosis, stroke, immune deficiencies resulting from bacterial, viral or  
CC fungal infection or from autoimmunity, cancer, allergy, asthma,  
CC graft-versus-host disease, eczema, haemophilia, thrombosis,  
CC anti-inflammatory diseases, nervous system disorders, and infection.  
CC The present sequence represents a protein of the invention.

**SQ Sequence 477 AA;**

Query Match	93.5%;	Score 2351.5;	DB 22;	Length 477;
Best Local Similarity	92.7%;	Pred. No. 4.9e-139;		
Matches 442;	Conservative 13;	Mismatches 19;	Indels 3;	Gaps 1

[illegible]

RESULT 4  
ABP58275

AC ABP58275;

DT 31-MAR-2003 (first entry)

DE Humanised 3D6 antibody heavy chain

KW Monoclonal antibody; 3D6; complementarity determining region; CDR;

KW Down's syndrome; cerebral amyloid angiopathy; neuroprotective;

XX

05 Chimeric - Homo sapiens.

FH	Key	Location
1	1	1
2	2	2
3	3	3
4	4	4
5	5	5
6	6	6
7	7	7
8	8	8
9	9	9
10	10	10
11	11	11
12	12	12
13	13	13
14	14	14
15	15	15
16	16	16
17	17	17
18	18	18
19	19	19
20	20	20
21	21	21
22	22	22
23	23	23
24	24	24
25	25	25
26	26	26
27	27	27
28	28	28
29	29	29
30	30	30
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98	98	98
99	99	99
100	100	100

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FT /label= Signal_peptide
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FT	/label= Mature_peptide

[illegible]

FT /note= "heavy chain variable region, claimed in

Region	50+.54
FT	

Region	FT
69.85	

FT	Region	118.127
----	--------	---------

[illegible]



PT useful for treating individual exposed to rabies virus and for  
 PT preventing spread of rabies virus to central nervous system -  
 PS Claim 4; Page 23-24; 25pp; English.

CC This sequence represents the heavy chain protein of the monoclonal  
 CC antibody from clone JA. The invention relates to an isolated human  
 CC monoclonal rabies virus neutralising antibody (vtrucide) derived from  
 CC cDNA clones encoding the antibody heavy and light chains expressed in  
 CC heterologous expression systems and purified away from deleterious  
 CC contaminants. The invention provides a fused gene encoding a chimeric  
 CC immunoglobulin light chain and a fused gene encoding a chimeric  
 CC immunoglobulin heavy chain. The antibody of the invention is useful for  
 CC treating an individual exposed to a rabies virus by administering to the  
 CC individual a therapeutically effective amount of the antibody, and  
 CC preventing a spread of the rabies virus to the central nervous system  
 CC (CNS). The antibody of the invention provides a safe and efficacious post  
 CC -exposure prophylactic therapy for individuals exposed to a rabies virus.  
 XX  
 XX  
 SO Sequence 474 AA;

Query Match 100.0%; Score 2514; DB 23; Length 474;  
 Best Local Similarity 100.0%; Pred. No. 3,4e-149;  
 Matches 474; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEFGLSMFLVAALKGVQCEVQLLESGGLVQPGSLRLSCAAGFTFSNYAMSWVRQAP 60  
 DB 1 MEFGLSMFLVAALKGVQCEVQLLESGGLVQPGSLRLSCAAGFTFSNYAMSWVRQAP 60  
 QY 61 GKLEWVSATISASGHSTYLDASVKGRTISDNSKNLTYLQMSLRADTAIVYYCANDRE 120  
 DB 61 GKLEWVSATISASGHSTYLDASVKGRTISDNSKNLTYLQMSLRADTAIVYYCANDRE 120  
 QY 121 VTMTVLVNGGFDYGGGRTVYVSASTKGPVFPFLAPSSKTSCTGTAALGCLVNDYPERP 180  
 DB 121 VTMTVLVNGGFDYGGGRTVYVSASTKGPVFPFLAPSSKTSCTGTAALGCLVNDYPERP 180  
 QY 181 VTMVNSGALTSVHTPRVAVLQSSGLVSLSSVTVPPSSSLGTQTYICNVNKKPSNTKYDK 240  
 DB 181 VTMVNSGALTSVHTPRVAVLQSSGLVSLSSVTVPPSSSLGTQTYICNVNKKPSNTKYDK 240  
 QY 241 RVEPKSCDKHTHTPCPCAPPELLGGPSVFLPFRPKDRLMTSRTEVTCVVVDVSHEDPEV 300  
 DB 241 RVEPKSCDKHTHTPCPCAPPELLGGPSVFLPFRPKDRLMTSRTEVTCVVVDVSHEDPEV 300  
 QY 301 KFNMYVDGVEVHNNAKTRPREQYNSTYRVYSVLTVLDHQMIDNGEKYCKVSNKALPAPIE 360  
 DB 301 KFNMYVDGVEVHNNAKTRPREQYNSTYRVYSVLTVLDHQMIDNGEKYCKVSNKALPAPIE 360  
 QY 361 KTISKAKGPREPOVYTLPSREEMTKNOVSLTCLVKGFTYPSDIAVEMESNGOPENNYKT 420  
 DB 361 KTISKAKGPREPOVYTLPSREEMTKNOVSLTCLVKGFTYPSDIAVEMESNGOPENNYKT 420  
 QY 421 TPPLVLDSDGSEFFLYSKLTVDKSRMQQGNVSCSYMHENLHNHYTQKSLSLSPGK 474  
 DB 421 TPPLVLDSDGSEFFLYSKLTVDKSRMQQGNVSCSYMHENLHNHYTQKSLSLSPGK 474

RESULT 2  
 AB08017  
 ID AB08017 standard; Protein: 474 AA.

AC AB08017;

XX 10-MAY-2003 (first entry)

DE Human monoclonal rabies virus antibody heavy chain, clone JH, protein.

XX Human; antibody; constant region; monoclonal antibody 57;

KM Mab 57; variable region; Rabies; neurological disease; infection;

KM central nervous system; rabies virus; lyssavirus; Rhabdoviridae;

KM pathogen; vaccine; virucide; heavy chain.

XX

OS Homo sapiens.

XX WO2003016501-A2.

XX 27-FEB-2003.

XX 21-AUG-2002; 2002WO-US26584.

XX 21-AUG-2001; 2001US-314023P.

XX (UYJE-) UNIV JEFFERSON THOMAS.

XX Hooper DC, Dietzschold B;

XX WPI: 2003-276566/27.

XX N-PSDB: ABX12855.

PT New recombinant antibody comprising a constant region of Mab 57 linked  
 PT to a non-Mab 57 variable region, useful for treating an individual  
 PT exposed to a pathogen, e.g. rabies infection -

XX Example 1; Page 32-33; 38pp; English.

CC The invention discloses a recombinant antibody comprising a constant  
 CC region of monoclonal antibody (Mab) 57 linked to a non-Mab 57 variable  
 CC region. Rabies is an acute, neurological disease caused by infection of  
 CC the central nervous system with the rabies virus, a member of the  
 CC Lyssavirus genus of the family Rhabdoviridae. Also disclosed are methods  
 CC for producing an isolated recombinant antibody by culturing a host cell,  
 CC containing a recombinant expression vector comprising the nucleic acid  
 CC molecule encoding the antibody, and isolating the recombinant antibody  
 CC expressed and treating an individual exposed to a pathogen by  
 CC administering to the individual the recombinant antibody. The recombinant  
 CC antibodies are useful for preventing (vaccine) and treating an individual  
 CC exposed to a pathogen, e.g. rabies infection. They are also useful for  
 CC the qualitative and quantitative determination of the rabies virus. The  
 CC sequences presented are the antibody protein fragments, the nucleic acids  
 CC encoding them or the PCR primers used to construct the recombinant  
 CC expression vector.

XX Sequence 474 AA;

Query Match 100.0%; Score 2514; DB 24; Length 474;  
 Best Local Similarity 100.0%; Pred. No. 3,4e-149;  
 Matches 474; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEFGLSMFLVAALKGVQCEVQLLESGGLVQPGSLRLSCAAGFTFSNYAMSWVRQAP 60  
 DB 1 MEFGLSMFLVAALKGVQCEVQLLESGGLVQPGSLRLSCAAGFTFSNYAMSWVRQAP 60  
 QY 61 GKLEWVSATISASGHSTYLDASVKGRTISDNSKNLTYLQMSLRADTAIVYYCANDRE 120  
 DB 61 GKLEWVSATISASGHSTYLDASVKGRTISDNSKNLTYLQMSLRADTAIVYYCANDRE 120  
 QY 121 VTMTVLVNGGFDYGGGRTVYVSASTKGPVFPFLAPSSKTSCTGTAALGCLVNDYPERP 180  
 DB 121 VTMTVLVNGGFDYGGGRTVYVSASTKGPVFPFLAPSSKTSCTGTAALGCLVNDYPERP 180  
 QY 181 VTMVNSGALTSVHTPRVAVLQSSGLVSLSSVTVPPSSSLGTQTYICNVNKKPSNTKYDK 240  
 DB 181 VTMVNSGALTSVHTPRVAVLQSSGLVSLSSVTVPPSSSLGTQTYICNVNKKPSNTKYDK 240  
 QY 241 RVEPKSCDKHTHTPCPCAPPELLGGPSVFLPFRPKDRLMTSRTEVTCVVVDVSHEDPEV 300  
 DB 241 RVEPKSCDKHTHTPCPCAPPELLGGPSVFLPFRPKDRLMTSRTEVTCVVVDVSHEDPEV 300  
 QY 301 KFNMYVDGVEVHNNAKTRPREQYNSTYRVYSVLTVLDHQMIDNGEKYCKVSNKALPAPIE 360  
 DB 301 KFNMYVDGVEVHNNAKTRPREQYNSTYRVYSVLTVLDHQMIDNGEKYCKVSNKALPAPIE 360  
 QY 361 KTISKAKGPREPOVYTLPSREEMTKNOVSLTCLVKGFTYPSDIAVEMESNGOPENNYKT 420  
 DB 361 KTISKAKGPREPOVYTLPSREEMTKNOVSLTCLVKGFTYPSDIAVEMESNGOPENNYKT 420

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OM protein - protein search, using sw model

Run on: September 12, 2003, 12:46:18 ; Search time 81.0085 Seconds  
(without alignments)  
928.747 Million cell updates/sec

Title: US-09-848-832-3

Perfect score: 2514  
Sequence: 1 MEFGLSWLFLVALILKGVCE.....MHEALNHXYTKSLSPK 474

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2514	100.0	474	23	AA014065 Heavy chain protel
2	2514	100.0	474	24	ABU08017 Human monoclonal r
3	2351.5	93.5	477	22	AAU14288 Human novel protei
4	2315	92.1	468	24	ABP58275 Humanised 3D6 anti
5	2309.5	91.7	475	13	AA020057 Heavy chain of 3D6
6	2304.5	91.7	461	22	AAU07745 Humanised monoclon
7	2279	90.7	449	21	AA568810 A rat heavy chain
8	2257	89.8	451	22	AAE12715 Human recombinant
9	2257	89.8	451	24	ABU58807 Mucin 1 (MUC-1) b1

10	2257	89.8	477	15	AAK47453	Ch1784.12 H3 heavy
11	2249.5	89.5	444	24	AAE34876	B17A4/8 antibody h
12	2244.5	89.3	447	24	AAE33522	Human AOC2 heavy c
13	2244.5	89.3	467	24	ABP71365	Anti-OPGL-1 antibo
14	2244	89.3	466	13	AAK24812	Sequence encoded b
15	2241	89.1	449	24	ABP58273	Humanised 3D6 anti
16	2238.5	89.0	447	23	AAE33523	Human AOC2 heavy c
17	2238	89.0	470	24	ABG77158	Germine protein s
18	2237.5	89.0	442	24	ABB80109	Heavy chain. Homo
19	2237.5	89.0	442	24	ABR39465	Humanised anti-Abe
20	2237.5	89.0	442	24	ABU08311	Humanised 266 anti
21	2235	88.9	468	23	ABU10365	Human breast speci
22	2234.5	88.9	447	24	AAE33524	Human AOC2 heavy c
23	2232.5	88.8	449	23	AAU18400	Mature humanised m
24	2226.5	88.6	442	24	ABB80113	Deglycosylated hea
25	2226.5	88.6	442	24	ABR39474	Humanised anti-Abe
26	2226.5	88.6	442	24	ABU08320	Humanised antibody
27	2221.5	88.4	459	14	AAK42066	Human anti-HBs hea
28	2221	88.3	464	23	ABG78151	Human antibody fra
29	2221	88.3	464	23	ABG91842	Human Fv molecule
30	2220	88.3	582	22	ABR81987	Ganglioside CD3 sp
31	2219	88.3	470	23	AAU81993	Amino acid sequenc
32	2218.5	88.2	519	23	AAU81993	Human secreted pro
33	2196	87.4	470	23	ABR81109	Anti-tissue factor
34	2196	87.4	470	24	ABP72748	Anti-tissue factor
35	2193.5	87.3	452	20	AAV29458	Recombinant immuno
36	2193.5	87.3	452	21	AAK30322	Humanised anti-IL-
37	2193.5	87.3	452	21	AAV77766	Humanised anti-IL-
38	2193.5	87.3	452	24	ABU59512	Humanised Mouse an
39	2193.5	87.3	452	24	ABU13799	Humanised mouse an
40	2188	87.0	470	23	ABG77161	Amino acid sequenc
41	2187.5	87.0	473	23	ABG77162	Germine protein s
42	2187	87.0	476	23	ABR81110	Anti-VEGF heavy ch
43	2184.5	86.9	452	19	AAK69316	Anti-IL-8 humanise
44	2183	86.8	478	19	AAK63763	Macaque primatized
45	2183	86.8	478	23	AAU11644	Protein sequence o

ALIGNMENTS

RESULT 1	
AA014065	AA014065 standard; Protein: 474 AA.
XX	XX
AC	AA014065:
XX	XX
DT	07-MAY-2002 (first entry)
XX	XX
DE	Heavy chain protein of the monoclonal antibody from clone JA.
XX	XX
KW	HRIG: human rabies-immune globulin; monoclonal; virucide; heavy chain;
KW	human monoclonal rabies virus neutralising antibody; immunoglobulin;
KW	light chain; central nervous system; CNS; prophylactic therapy; clone JA.
OS	Homo sapiens.
XX	XX
PN	WO200188132-A2.
XX	XX
PD	22-NOV-2001.
XX	XX
PF	04-MAY-2001; 2001WO-US14468.
XX	XX
PR	16-MAY-2000; 2000US-204518P.
XX	XX
PA	(UYJE-) UNIV JEFFERSON THOMAS.
XX	XX
PI	Hooper DC, Dietzschold B.
XX	XX
DR	WPI: 2002-062381/08.
DR	N-PSDB; AAK98701.
XX	XX
PT	Novel isolated human monoclonal rabies virus neutralising antibody

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OM protein - protein search, using sw model

Run on: September 12, 2003, 13:00:49 : Search time 15.2034 Seconds  
(without alignments)  
2245.783 Million cell updates/sec

Title: US-09-848-832-4

Perfect score: 1223

Sequence: 1 MEAPAQQLFLLLMLPDTTG.....EVTHGGLSSPYTKSPNRGEC 234

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 541936 seqs, 145912426 residues

Total number of hits satisfying chosen parameters: 541936

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*  
14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*  
15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*  
17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*  
18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1223	100.0	234	US-10-225-108A-4	Sequence 4, Appli
2	1223	100.0	234	US-09-848-832-4	Sequence 4, Appli
3	1108.5	90.6	235	US-10-153-382-7	Sequence 7, Appli
4	1096	89.6	233	US-10-153-382-15	Sequence 15, Appli
5	1085.5	88.8	234	US-10-153-382-11	Sequence 11, Appli
6	1076	88.0	236	US-09-859-053-34	Sequence 34, Appli
7	1066	87.2	236	US-09-859-053-38	Sequence 38, Appli
8	1057	86.4	224	US-09-453-234-82	Sequence 82, Appli
9	1057	86.4	224	US-09-453-234-88	Sequence 88, Appli
10	1057	86.4	224	US-09-453-234-90	Sequence 90, Appli
11	1054	86.2	224	US-09-453-234-36	Sequence 36, Appli
12	1045	85.4	224	US-09-453-234-84	Sequence 84, Appli
13	1043	85.3	224	US-09-453-234-46	Sequence 46, Appli
14	1027	84.0	238	US-10-216-484-107	Sequence 107, App
15	1015	83.0	236	US-09-859-053-30	Sequence 30, Appli

16	1015	83.0	238	US-10-216-484-50	Sequence 50, Appli
17	1009.5	82.5	241	US-10-221-945-1	Sequence 1, Appli
18	999	81.7	238	US-10-216-484-109	Sequence 109, App
19	997	81.5	238	US-10-216-484-129	Sequence 129, App
20	994	81.3	238	US-10-216-484-131	Sequence 131, App
21	993	81.2	234	US-09-740-002-24	Sequence 24, Appli
22	993	81.2	238	US-10-216-484-52	Sequence 52, Appli
23	993	81.2	238	US-10-216-484-127	Sequence 127, App
24	991	81.0	215	US-09-791-153A-47	Sequence 47, Appli
25	987	80.7	226	US-09-453-234-74	Sequence 74, Appli
26	986	80.6	212	US-10-006-593-118	Sequence 118, App
27	985	80.5	228	US-09-453-234-86	Sequence 86, Appli
28	985	80.5	238	US-10-216-484-54	Sequence 54, Appli
29	984.5	80.5	215	US-09-972-656-100	Sequence 100, App
30	983.5	80.5	239	US-09-249-011A-72	Sequence 22, Appli
31	982	80.3	226	US-09-453-234-50	Sequence 50, Appli
32	982	80.3	226	US-09-453-234-80	Sequence 80, Appli
33	982	80.3	240	US-10-159-006-36	Sequence 36, Appli
34	981.5	80.3	234	US-10-026-925-55	Sequence 55, Appli
35	980	80.1	226	US-09-453-234-38	Sequence 38, Appli
36	977	79.9	224	US-09-453-234-52	Sequence 52, Appli
37	976	79.8	226	US-09-453-234-42	Sequence 42, Appli
38	976	79.8	236	US-10-006-593-69	Sequence 69, Appli
39	975.5	79.8	213	US-10-150-475A-4	Sequence 4, Appli
40	973	79.6	224	US-09-453-234-44	Sequence 44, Appli
41	973	79.6	224	US-09-453-234-78	Sequence 78, Appli
42	972	79.5	224	US-09-453-234-40	Sequence 40, Appli
43	972	79.5	226	US-09-453-234-72	Sequence 72, Appli
44	970	79.3	238	US-10-171-452A-38	Sequence 38, Appli
45	970	79.3	238	US-10-171-452A-56	Sequence 56, Appli

## ALIGNMENTS

RESULT 1	US-10-225-108A-4
Sequence 4, Application US/10225108A	
Publication No. US20030157112A1	
GENERAL INFORMATION:	
APPLICANT: HOOVER, Craig	
APPLICANT: DIETZSCHOLD, Bernhard	
TITLE OF INVENTION: Recombinant Antibodies, and Compositions	
TITLE OF INVENTION: and Methods for Making Them	
FILE REFERENCE: 8321-110	
CURRENT APPLICATION NUMBER: US/10/225,108A	
CURRENT FILING DATE: 2003-04-10	
PRIOR APPLICATION NUMBER: US 09/848, 832	
PRIOR FILING DATE: 2001-05-04	
PRIOR APPLICATION NUMBER: US 60/204,518	
PRIOR FILING DATE: 2001-05-16	
PRIOR APPLICATION NUMBER: US 60/314,023	
PRIOR FILING DATE: 2001-08-21	
NUMBER OF SEQ ID NOS: 16	
SOFTWARE: FastSeq for Windows Version 4.0	
SEQ ID NO 4	
LENGTH: 234	
TYPE: PRT	
ORGANISM: Homo sapiens	
US-10-225-108A-4	
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Best Local Similarity	100.0%: Pred. No. 1.2e72:
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QY	61 GQAPRLIYDTSNRATGIPARFSGSGGDTFTLSSLE:EDPFAVYCCOQRNMPWTFQ 120
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Oy 121 GTKVEFKRTVAAPSVFIPEPSDEQLKSGTASVCLNNFYPREAKVQMKVDNALQSGNSQ 180  
Db 121 GTKVEFKRTVAAPSVFIPEPSDEQLKSGTASVCLNNFYPREAKVQMKVDNALQSGNSQ 180  
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Db 181 ESVTEODSKDSTYSLSTLTLSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 234

## RESULT 2

US-09-848-832-4  
; Sequence 4, Application US/09848832  
; Publication No. US20030165507A1  
; GENERAL INFORMATION:  
; APPLICANT: Hooper, Douglas  
; TITLE OF INVENTION: RABIES VIRUS-SPECIFIC NEUTRALIZING HUMAN  
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND NUCLEIC ACIDS AND RELATED METHODS  
; FILE REFERENCE: H0001.NP0002  
; CURRENT FILING DATE: 2001-05-04  
; PRIOR APPLICATION NUMBER: 60/204,518  
; PRIOR FILING DATE: 2000-05-16  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 234  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-848-832-4

Query Match 100.0%; Score 1223; DB 12; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1,2e-72;  
Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MEAPAOQLFLLLMLPDTTGEIVLTOSPATLSLSPGERATLACRASQTSRYLAWYQOKP 60  
Db 1 MEAPAOQLFLLLMLPDTTGEIVLTOSPATLSLSPGERATLACRASQTSRYLAWYQOKP 60  
Oy 61 GOAPRLIYDTSNRATGIPARFSGSGCTDFTLSTLSLEPDPFVYYCOQRFNMPWTFGQ 120  
Db 61 GOAPRLIYDTSNRATGIPARFSGSGCTDFTLSTLSLEPDPFVYYCOQRFNMPWTFGQ 120  
Oy 121 GTKVEFKRTVAAPSVFIPEPSDEQLKSGTASVCLNNFYPREAKVQMKVDNALQSGNSQ 180  
Db 121 GTKVEFKRTVAAPSVFIPEPSDEQLKSGTASVCLNNFYPREAKVQMKVDNALQSGNSQ 180  
Oy 181 ESVTEODSKDSTYSLSTLTLSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 234  
Db 181 ESVTEODSKDSTYSLSTLTLSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 234

## RESULT 3

US-10-153-382-7  
; Sequence 7, Application US/10153382  
; Publication No. US20030086930A1  
; GENERAL INFORMATION:  
; APPLICANT: PEIZER PRODUCTS INC.  
; TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES  
; FILE REFERENCE: PC23019A  
; CURRENT APPLICATION NUMBER: US/10/153,382  
; CURRENT FILING DATE: 2002-05-22  
; PRIOR APPLICATION NUMBER: 60/293042  
; PRIOR FILING DATE: 2001-05-23  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 235  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-153-382-7

Query Match 90.6%; Score 1108.5; DB 15; Length 235;

Best Local Similarity 91.5%; Pred. No. 3.5e-65;  
Matches 215; Conservative 7; Mismatches 12; Indels 1; Gaps 1;

Oy 1 MEAPAOQLFLLLMLPDTTGEIVLTOSPATLSLSPGERATLACRASQTSRYLAWYQOKP 59  
Db 1 MEAPAOQLFLLLMLPDTTGEIVLTOSPATLSLSPGERATLACRASQTSRYLAWYQOKP 60  
Oy 60 GOAPRLIYDTSNRATGIPARFSGSGCTDFTLSTLSLEPDPFVYYCOQRFNMPWTFG 119  
Db 60 GOAPRLIYDTSNRATGIPARFSGSGCTDFTLSTLSLEPDPFVYYCOQRFNMPWTFG 120  
Oy 120 OGTKEFKRTVAAPSVFIPEPSDEQLKSGTASVCLNNFYPREAKVQMKVDNALQSGNS 179  
Db 120 OGTKEFKRTVAAPSVFIPEPSDEQLKSGTASVCLNNFYPREAKVQMKVDNALQSGNS 180  
Oy 180 ESVTEODSKDSTYSLSTLTLSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 234  
Db 180 ESVTEODSKDSTYSLSTLTLSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 235

## RESULT 4

US-10-153-382-15  
; Sequence 15, Application US/10153382  
; Publication No. US20030086930A1  
; GENERAL INFORMATION:  
; APPLICANT: PEIZER PRODUCTS INC.  
; TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES  
; FILE REFERENCE: PC23019A  
; CURRENT APPLICATION NUMBER: US/10/153,382  
; CURRENT FILING DATE: 2002-05-22  
; PRIOR APPLICATION NUMBER: 60/293042  
; PRIOR FILING DATE: 2001-05-23  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 15  
; LENGTH: 234  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-153-382-15

Query Match 89.6%; Score 1096; DB 15; Length 234;  
Best Local Similarity 91.0%; Pred. No. 2.3e-64;  
Matches 213; Conservative 6; Mismatches 15; Indels 0; Gaps 0;

Oy 1 MEAPAOQLFLLLMLPDTTGEIVLTOSPATLSLSPGERATLACRASQTSRYLAWYQOKP 60  
Db 1 MEAPAOQLFLLLMLPDTTGEIVLTOSPATLSLSPGERATLACRASQTSRYLAWYQOKP 60  
Oy 61 GOAPRLIYDTSNRATGIPARFSGSGCTDFTLSTLSLEPDPFVYYCOQRFNMPWTFGQ 120  
Db 61 GOAPRLIYDTSNRATGIPARFSGSGCTDFTLSTLSLEPDPFVYYCOQRFNMPWTFGQ 120  
Oy 121 GTKVEFKRTVAAPSVFIPEPSDEQLKSGTASVCLNNFYPREAKVQMKVDNALQSGNSQ 180  
Db 121 GTKVEFKRTVAAPSVFIPEPSDEQLKSGTASVCLNNFYPREAKVQMKVDNALQSGNSQ 180  
Oy 181 ESVTEODSKDSTYSLSTLTLSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 234  
Db 181 ESVTEODSKDSTYSLSTLTLSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 234

## RESULT 5

US-10-153-382-11  
; Sequence 11, Application US/10153382  
; Publication No. US20030086930A1  
; GENERAL INFORMATION:  
; APPLICANT: PEIZER PRODUCTS INC.  
; TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES  
; FILE REFERENCE: PC23019A  
; CURRENT APPLICATION NUMBER: US/10/153,382  
; CURRENT FILING DATE: 2002-05-22  
; PRIOR APPLICATION NUMBER: 60/293042  
; PRIOR FILING DATE: 2001-05-23

NUMBER OF SEQ ID NOS: 39  
 SOFTWARE: Patentln Ver. 2.1  
 SEQ ID NO 11  
 LENGTH: 233  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-153-382-11

Query Match 88.8%; Score 1085.5; DB 15; Length 233;  
 Best Local Similarity 91.0%; Pred. No. 1.1e-63;  
 Matches 213; Conservative 5; Mismatches 15; Indels 1; Gaps 1;

QY 1 MEAPQALLFLLLMLPDTTGEIVLTQSPATLSLSPGERATLACRASQTASRYLAWYQOKP 60  
 DB 1 METPAQLLFLLMLPDTTGEIVLTQSPETLSLSPGERATLSCRNS-VSSSLAWYQOKP 59  
 QY 61 GOAPRLLYDTSNRATGIPARFSGSGSTDTFTLSISLEPEDFAVYYCQQRNMPWTFQ 120  
 DB 60 GOAPRLLYGASSRATGIPDRFSGSGSTDTFTLTISRLEPEDFAVYYCQYGISPTFGG 119  
 QY 121 GTKVEFKRTVAAPSVFIFPPSDEOLKSGTASVCLLNNFYPREAKVOMKVDNALQSGNSQ 180  
 DB 120 GTKVEIKRTVAAPSVFIFPPSDEOLKSGTASVCLLNNFYPREAKVOMKVDNALQSGNSQ 179  
 QY 181 ESVTEQDSKSDSTYSLSTLTLSKADYEEKHKVYACEVTHQGLSSPYTKSFNRGEC 234  
 DB 180 ESVTEQDSKSDSTYSLSTLTLSKADYEEKHKVYACEVTHQGLSSPYTKSFNRGEC 233

RESULT 6  
 US-09-859-053-34  
 Sequence 34, Application US/09859053  
 Patent No. US20020102658A1

GENERAL INFORMATION:  
 APPLICANT: Tsuji, Takashi  
 APPLICANT: Tezuka, Katsunari  
 APPLICANT: Horii, No. US20020102658A1uaki  
 TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A  
 TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND  
 TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF  
 FILE REFERENCE: 06501-079001  
 CURRENT APPLICATION NUMBER: US/09/859,053  
 CURRENT FILING DATE: 2001-05-16  
 PRIOR APPLICATION NUMBER: JP 2001-99508  
 PRIOR FILING DATE: 2001-03-30  
 PRIOR APPLICATION NUMBER: JP 2000-147116  
 PRIOR FILING DATE: 2000-05-18  
 NUMBER OF SEQ ID NOS: 43  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 34  
 LENGTH: 236  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-859-053-34

Query Match 88.0%; Score 1076; DB 10; Length 236;  
 Best Local Similarity 90.3%; Pred. No. 4.6e-63;  
 Matches 213; Conservative 6; Mismatches 15; Indels 2; Gaps 2;

QY 1 MEAPQALLFLLLMLPDTTGEIVLTQSPATLSLSPGERATLACRASQT-ASRYLAWYQOK 59  
 DB 1 METPAQLLFLLMLPDTTGEIVLTQSPETLSLSPGERATLSCRASQNTSRSSYLAWYQOK 60  
 QY 60 PGQARLLIYDTSNRATGIPARFSGSGSTDTFTLSISLEPEDFAVYYCQQRNMPW-TF 118  
 DB 61 PGQAGLLIYGASSRATGIPDRFSGSGSTDTFTLTISRLEPEDFAVYYCQQRNMPW-TF 120  
 QY 119 GOGTVEFKRTVAAPSVFIFPPSDEOLKSGTASVCLLNNFYPREAKVOMKVDNALQSGN 178  
 DB 121 GOGTLEIKRTVAAPSVFIFPPSDEOLKSGTASVCLLNNFYPREAKVOMKVDNALQSGN 180  
 QY 179 SOESTVEDSKSDSTYSLSTLTLSKADYEEKHKVYACEVTHQGLSSPYTKSFNRGEC 234  
 DB 179 SOESTVEDSKSDSTYSLSTLTLSKADYEEKHKVYACEVTHQGLSSPYTKSFNRGEC 234

DB 181 SOESTVEDSKSDSTYSLSTLTLSKADYEEKHKVYACEVTHQGLSSPYTKSFNRGEC 236

RESULT 7  
 US-09-859-053-38  
 Sequence 38, Application US/09859053  
 Patent No. US20020102658A1

GENERAL INFORMATION:  
 APPLICANT: Tsuji, Takashi  
 APPLICANT: Tezuka, Katsunari  
 APPLICANT: Horii, No. US20020102658A1uaki  
 TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A  
 TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND  
 TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF  
 FILE REFERENCE: 06501-079001  
 CURRENT APPLICATION NUMBER: US/09/859,053  
 CURRENT FILING DATE: 2001-05-16  
 PRIOR APPLICATION NUMBER: JP 2001-99508  
 PRIOR FILING DATE: 2001-03-30  
 PRIOR APPLICATION NUMBER: JP 2000-147116  
 PRIOR FILING DATE: 2000-05-18  
 NUMBER OF SEQ ID NOS: 43  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 38  
 LENGTH: 236  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-859-053-38

Query Match 87.2%; Score 1066; DB 10; Length 236;  
 Best Local Similarity 89.4%; Pred. No. 2e-62;  
 Matches 211; Conservative 9; Mismatches 14; Indels 2; Gaps 2;

QY 1 MEAPQALLFLLLMLPDTTGEIVLTQSPATLSLSPGERATLACRASQT-ASRYLAWYQOK 59  
 DB 1 METPAQLLFLLMLPDTTGEIVLTQSPETLSLSPGERATLSCRASQNTSRSSYLAWYQOK 60  
 QY 60 PGQARLLIYDTSNRATGIPARFSGSGSTDTFTLSISLEPEDFAVYYCQQRNMPW-TF 118  
 DB 61 PGQAGLLIYGASSRATGIPDRFSGSGSTDTFTLTISRLEPEDFAVYYCQQRNMPW-TF 120  
 QY 119 GOGTVEFKRTVAAPSVFIFPPSDEOLKSGTASVCLLNNFYPREAKVOMKVDNALQSGN 178  
 DB 121 GOGTLEIKRTVAAPSVFIFPPSDEOLKSGTASVCLLNNFYPREAKVOMKVDNALQSGN 180  
 QY 179 SOESTVEDSKSDSTYSLSTLTLSKADYEEKHKVYACEVTHQGLSSPYTKSFNRGEC 234  
 DB 181 SOESTVEDSKSDSTYSLSTLTLSKADYEEKHKVYACEVTHQGLSSPYTKSFNRGEC 236

RESULT 8  
 US-09-453-234-82  
 Sequence 82, Application US/09453234  
 Publication No. US20030091995A1

GENERAL INFORMATION:  
 APPLICANT: Buechler, Joe  
 APPLICANT: Walkers, Gunars  
 APPLICANT: Gray, Jeff  
 APPLICANT: Lomborg, Nils  
 APPLICANT: Biosite Diagnostics, Inc.  
 APPLICANT: Genpharm International  
 TITLE OF INVENTION: Human Antibodies  
 FILE REFERENCE: 020015-000110US  
 CURRENT APPLICATION NUMBER: US/09/453,234  
 CURRENT FILING DATE: 1999-12-01  
 PRIOR APPLICATION NUMBER: US 60/157,415  
 PRIOR FILING DATE: 1999-10-02  
 NUMBER OF SEQ ID NOS: 112  
 SOFTWARE: Patentln Ver. 2.1  
 SEQ ID NO 82  
 LENGTH: 224  
 TYPE: PRT  
 ORGANISM: Homo sapiens

OTHER INFORMATION: M2-31L  
US-09-453-234-82

Query Match	86.4%	Score 1057	DB 11	Length 224
Best Local Similarly	95.8%	Pred. No. 7.5e-62		
Matches 204	Conservative 3	Mismatches 6	Indels 0	Gaps 0

Qy	2	EIVLTOSPPATLSISPERATLACRASQTSRXLVIAOQKPCOAPBLLYDTSNATGIPA	80
Dd	1	EIVLTOSPPATLSISPERATLTCRASQTSVSTLVAQKPCOAPBLLYDASNATGIPA	60
Qy	81	RFSGSGSGDTFTLSISLEPEDFAVYYCOQRFNMFWTEGCGTKVEFKRTVAAPSVFTFPP	140
Dd	61	RFGSGSGSGDTFTLTSSLEPEDFAVYYCOQRFNMFWTEGCGTKVEIKRTVAAPSVFTFPP	120
Qy	141	SDEQLKSGTASVYCCLLINFTYPREAKVQMKVDNALSGNSQSVTEBODSKDSTYLSSTLT	200
Dd	121	SDEQLKSGTASVYCCLLINFTYPREAKVQMKVDNALSGNSQSVTEBODSKDSTYLSSTLT	180
Qy	201	LSKADYEKKHKVYACEVTHQGLSSPYTKSNRGE	233
Dd	181	LSKADYEKKHKVYACEVTHQGLSSPYTKSNRGE	213

RESULT 9  
US-09-453-234-88

; Sequence 88, Application US/09453234  
; Publication No. US20030091995A1

```

1  GENERAL INFORMATION:
2  APPLICANT: Buechler, Joe
3  APPLICANT: Valtris, Gunnars
4  APPLICANT: Gray, Jeff
5  APPLICANT: Lomberg, Nils
6  APPLICANT: Biosite Diagnostics, Inc.
7  APPLICANT: Genpharm International
8  TITLE OF INVENTION: Human Antibodies
9  FILE REFERENCE: 020015-000110US
10 CURRENT APPLICATION NUMBER: US/09/453,233
11 PRIORITY FILING DATE: 1999-12-01
12 PRIOR APPLICATION NUMBER: US 60/157,415
13 PRIOR FILING DATE: 1999-10-02
14 NUMBER OF SEQ ID NOS: 112
15 SOFTWARE: PatentIn Ver. 2.1
16 SEQ ID NO 88
17 LENGTH: 224
18 TYPE: prt
19 ORGANISM: Homo sapiens
20 OTHER INFORMATION: M2-34L
21 US-09-453-234-88

```

Query Match	86.4%	Score 1057	DB 11	Length 224
Best Local Similarity	95.8%	Pred. No. 7.5e62		
Matches 204	Conservative	3	Mismatches 6	Indels 0
				Gaps 0

QY	2	EIVLTDSPTLSSIPERATLTACRASQASRIAMYOQKPCQAPRLLIYDTSNATGIPA	80
Db	1	EIVLTDSPTLSSIPERATLTACRASQASSTIAMIYQKPCQAPRLLIYDASNATGIPA	60
QY	81	REFSGSGSDFTLTLSISLEPEDFAVYYCCQGRFNMPTFGGTAKYEFKRTVAAPSVFIFPP	140
Db	61	REFSGSGSGDFTLTLTSSLEPEDFAVYYCCQGRFMNPTFGGTAKYIKRTVAAPSVFIFPP	120
QY	141	SDEQLKSGTASVYVCLLNFFYPREAKVQMKVDNALQSGNSQESVTEEDSDKSTYSLSSTLT	200
Db	121	SDEQLKSGTASVYVCLLNFFYPREAKVQMKVDNALQSGNSQESVTEEDSDKSTYSLSSTLT	180
QY	201	LSKADYEKHKVYACETVHQGLSSPTKSPFNQGE	233
Db	181	LSKADYEKHKVYACETVHQGLSSPTKSPFNQGE	213

RESULT 10  
US-09-453-234-90

; Sequence 90, Application US/09453234  
; Publication No. US20030091995A1

```

1  GENERAL INFORMATION:
2  APPLICANT: Buechler, Joe
3  APPLICANT: Valkirs, Gunars
4  APPLICANT: Gray, Jeff
5  APPLICANT: Lomborg, Nils
6  APPLICANT: Bioste Diagnostics, Inc.
7  APPLICANT: Genpharm International
8  TITLE OF INVENTION: Human Antibodies
9  FILE REFERENCE: 020015-000110US
10 CURRENT APPLICATION NUMBER: US/09/453,233
11 PRIORITY FILING DATE: 1999-12-01
12 PRIOR APPLICATION NUMBER: US 60/157,415
13 PRIOR FILING DATE: 1999-10-02
14 NUMBER OF SEQ ID NOS: 112
15 SOFTWARE: PatentIn Ver. 2.1
16 SEQ ID NO 90
17 LENGTH: 224
18 TYPE: prt
19 ORGANISM: Homo sapiens
20 OTHER INFORMATION: M2-55L
21 US-09-453-234-90

```

Query Match	86.4%	Score 1057	DB 11	Length 224
Best Local Similarly	95.8%	Pred. No. 7.5e 62		
Matches 204	Conservative	3	Mismatches 6	Indels 0
				Gaps 0

```

QY      2 EIVLTOSPATLSLSPERRATLACRSASQVTSFLAYAOQPCQAPRLLIYDTSNATGIPA 80
Db      1 EIVLTOSPATLSLSPERRATLSCRASQSVSTLIAYOQPCQAPRLLIYDASNATGIPA 60

QY      81 RFSGSGSGNDFTLSSLEPEDFAVYYCOQRFNMPFTEGCGTKVEFKRTVAAPSVFIIPP 140
Db      61 RFSGSGSGNDFTLTISLEPEDFAVYYCOQRFNMPFRTGGCGKVEIKRTVAAPSVFIIPP 120

QY      141 SDEQLKSGTASVYCLINNFYPREAKVOMKVNDALOGSOSQSVYBODSKDSTVLSSTLT 200
Db      121 SDEQLKSGTASVYCLINNFYPREAKVOMKVNDALOGSOSQSVYBODSKDSTVLSSTLT 180

QY      201 LSKADYEKKHKVYACEVTHOGLSSPYTKSNRGE 233
Db      181 LSKADYEKKHKVYACEVTHOGLSSPYTKSNRGE 213

```

## RESULT 11

US-09-453-234-36  
; Sequence 36, Application US/09453234  
; Publication No. US20030091995A1

```

1  GENERAL INFORMATION:
2  APPLICANT: Buechler, Joe
3  APPLICANT: Valakis, Guinars
4  APPLICANT: Gray, Jeff
5  APPLICANT: Lomborg, Mills
6  APPLICANT: Biosite Diagnostics, Inc.
7  APPLICANT: Genpharm International
8  TITLE OF INVENTION: Human Antibodies
9  FILE REFERENCE: 020015-00011005
10 CURRENT APPLICATION NUMBER: US/09/453,234
11 CURRENT FILING DATE: 1999-12-01
12 PRIOR APPLICATION NUMBER: US 60/157,415
13 PRIOR FILING DATE: 1999-10-02
14 NUMBER OF SEQ ID NOS: 112
15 SOFTWARE: PatentIn Ver. 2.1
16 SEQ ID NO 36
17
18 LENGTH: 224
19
20 TYPE: PRT
21 ORGANISM: Homo sapiens
22
23 US-09-453-234 -36

```

Query Match	86.28	Score 1054	DB 11	Length 224
Best Local Similarity	95.88	Pred. No. 1.2e-61		
Matches 204; Conservative	2	Mismatches	7	Indels 0
				Gaps 0

[illegible]

```

RESULT 12
US-09-453-234-84
: Sequence 84, Application US/09453234
: Publication NO. US20030091995A1
: GENERAL INFORMATION:
: APPLICANT: Buechler, Joe
: APPLICANT: Valkirs, Gunars
: APPLICANT: Gray, Jeff
: APPLICANT: Lonberg, Nils
: APPLICANT: Biosite Diagnostics, Inc.
: APPLICANT: Genpharm International
: TITLE OF INVENTION: Human Antibodies
: FILE REFERENCE: 020015-00011005
: CURRENT APPLICATION NUMBER: US/09/453,234
: CURRENT FILING DATE: 1999-12-01
: PRIOR APPLICATION NUMBER: US 60/157,415
: PRIOR FILING DATE: 1999-10-02
: NUMBER OF SEQ ID NOS: 112
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 84
: LENGTH: 224
: TYPE: PRY
: ORGANISM: Homo sapiens
: OTHER INFORMATION: M2-32L
US-09-453-234-84

```

[illegible]

```

: APPLICANT: Lonberg, Nils
: APPLICANT: Biosite Diagnostics, Inc.
: APPLICANT: GenPharm International
: TITLE OF INVENTION: Human Antibodies
: FILE REFERENCE: 020015-000110US
: CURRENT APPLICATION NUMBER: US/09/453,234
: CURRENT FILING DATE: 1999-12-01
: PRIOR APPLICATION NUMBER: US 60/157,415
: PRIOR FILING DATE: 1999-10-02
: NUMBER OF SEQ ID NOS: 112
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 46
: LENGTH: 224
: TYPE: PRT
: ORGANISM: Homo sapiens
: OTHER INFORMATION: MI-10L
: US-09-453-234-46

```

[illegible]

RESULT 14  
US-10-216-484-107  
Sequence 107, Application US/10216484  
Publication No. US20030103976A1  
GENERAL INFORMATION:  
APPLICANT: Serizawa, NO. US20030103976A1ufusa  
APPLICANT: Haruyama, Hideyuki  
APPLICANT: Nakahara, Kaori  
APPLICANT: Tamaki, Ikuko  
APPLICANT: Takahashi, Toru  
TITLE OF INVENTION: Anti-Pas Antibodies  
FILE REFERENCE: 980126CIP/HG  
CURRENT APPLICATION NUMBER: US/10/216,484  
CURRENT FILING DATE: 2002-08-09  
PRIOR APPLICATION NUMBER: US/09/499,662  
PRIOR FILING DATE: 2000-02-09  
PRIOR APPLICATION NUMBER: US 09/053,583  
PRIOR FILING DATE: 1998-04-01  
NUMBER OF SEQ ID NOS: 165  
SEQ ID NO 107  
LENGTH: 238  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Designed light  
OTHER INFORMATION: chain of humanized anti-Pas antibody  
US-10-216-484-107

Query Match	84.0%;	Score 1027;	DB 15;	Length 238;
Best Local Similarity	84.5%;	Pred. No. 7.1e-60;		
Matches 201;	Conservative 11;	Mismatches 22;	Indels 4;	Gaps 1

  

Oy	1	MEADPQLLELLMLPDTGTGELVLTQSPATISLSGERATVACRA	SQT---	ASRYLAWY	56



```
Db      1 METDTILLMVLWPGSTGEIVLTQSPGTLSPGERATLSCKASQGVVDYDGSYNNMY 60
OY      57 QOKPGQAPRLIYDTSNRATGIPARFSGSGGTDEFTLSSLEPEDFAVYYCCOQRFNMPW 116
        ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      61 QOKPGQAPRLIYASNIIESGIPDRFSGSGGTDEFTLISRLPEPDFAVYYCCOQSNEDPR 120
OY      117 TEGGCTKVEFRKTVAAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQKVDNALQS 176
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      121 TEGGCTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQKVDNALQS 180
OY      177 GNSQESVTEODSKDSTYSLSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 234
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      181 GNSQESVTEODSKDSTYSLSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 238
```

## RESULT 15

```
US-09-859-053-30
: Sequence 30, Application US/09859053
: Patent No. US20020102658A1
: GENERAL INFORMATION:
: APPLICANT: Tezuka, Takashi
: APPLICANT: Hori, No US20020102658A1uaki
: TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
: TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE ALLIM AND
: FILE REFERENCE: 06501-079001
: CURRENT APPLICATION NUMBER: US/09/859, 053
: PRIOR FILING DATE: 2001-05-16
: PRIOR APPLICATION NUMBER: JP 2001-99508
: PRIOR FILING DATE: 2001-03-30
: PRIOR APPLICATION NUMBER: JP 2000-147116
: NUMBER OF SEQ ID NOS: 43
: SOFTWARE: fastseq for Windows Version 4.0
: SEQ ID NO 30
: LENGTH: 236
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-859-053-30
```

```
Query Match      83.0%; Score 1015; DB 10; Length 236;
Best Local Similarity 82.5%; Pred. No. 4.3e-59;
Matches 193; Conservative 18; Mismatches 23; Indels 0; Gaps 0;
```

```
OY      1 MEAPAOILFLLLMLPDTGTGIVLTQSPATLSLSPGERATLACRASQTSARYLAMYQOKP 60
        | ||||| ||||| ||| : ||||| : ||| : ||||| || ||||| |||||
Db      3 MRVPAQLGLGLLMLPFGSRCDIQMTQSPSSVSASVGDRTVITCRASQGISRLAWYQOKP 62
OY      61 GOAPRLIYDTSNRATGIPARFSGSGGTDEFTLSSLEPEDFAVYYCCOQRFNMPWTFGQ 120
        ||||| ||| : ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      63 GKAPRLIYASNIIESGIPDRFSGSGGTDEFTLISRLPEPDFAVYYCCOQNSFPWTFGQ 122
OY      121 GTKVEFRKTVAAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQKVDNALQSGNSQ 180
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      123 GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQKVDNALQSGNSQ 182
OY      181 ESVTEODSKDSTYSLSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 234
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      183 ESVTEODSKDSTYSLSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 236
```

Search completed: September 12, 2003, 13:06:07  
Job time : 16.2034 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 12, 2003, 12:58:39 ; Search time 13.2203 Seconds  
(without alignments)  
748.902 Million cell updates/sec

Title: US-09-848-832-4

Perfect score: 1223

Sequence: 1 MEAPRQLLEFLLLMLPDTTG.....EYTHGGLSSPTKSRNGEC 234

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep:\*
- 2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep:\*
- 3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep:\*
- 4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep:\*
- 5: /cgn2\_6/ptodata/1/1aa/PCRTUS\_COMB.pep:\*
- 6: /cgn2\_6/ptodata/1/1aa/Backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1056	86.3	234	3	US-09-049-672A-6
2	993	81.2	234	4	US-09-740-002-24
3	982	80.3	240	4	US-09-301-593-36
4	978.5	80.0	235	1	US-08-276-852-153
5	978.5	80.0	235	1	US-08-899-575-153
6	978.5	80.0	235	1	US-08-899-575-153
7	978.5	80.0	235	5	PCR-US95-08743-153
8	978	80.0	235	4	US-08-812-586-16
9	978	80.0	235	4	US-09-535-832A-17
10	970.5	79.4	241	2	US-07-916-098A-56
11	962.5	78.7	214	2	US-08-480-753-6
12	962.5	78.7	214	3	US-09-041-889-11
13	962.5	78.7	214	3	US-08-837-058-11
14	962.5	78.7	214	4	US-09-417-264-11
15	962.5	78.7	236	4	US-09-315-926A-79
16	955.5	78.1	239	3	US-08-487-550-6
17	955.5	78.1	239	4	US-09-526-098-6
18	955	78.1	236	4	US-08-157-101A-5
19	954.5	78.0	233	4	US-09-485-737B-69
20	946.5	77.4	235	3	US-09-171-945-97
21	946	77.4	214	1	US-08-458-516-12
22	945.5	77.3	234	4	US-09-740-002-26
23	944	77.2	232	1	US-08-704-744-80
24	942	77.0	218	5	PCR-US96-13152-2
25	941.5	77.0	233	4	US-09-301-593-28
26	941.5	77.0	233	2	US-07-934-373C-25
27	941.5	77.0	233	3	US-08-437-642B-25

28	941.5	77.0	233	4	US-08-146-206C-25	Sequence 25, Appl
29	941.5	77.0	233	5	PCR-US93-07832-25	Sequence 25, Appl
30	941	76.9	215	2	US-08-480-753-8	Sequence 8, Appl1
31	938	76.7	214	2	US-07-934-373C-39	Sequence 39, Appl
32	938	76.7	214	3	US-08-437-642B-39	Sequence 39, Appl
33	938	76.7	214	5	PCR-US93-07832-39	Sequence 39, Appl
34	937	76.6	214	2	US-07-934-373C-40	Sequence 40, Appl
35	937	76.6	214	2	US-08-788-800-11	Sequence 11, Appl
36	937	76.6	214	3	US-08-437-642B-40	Sequence 40, Appl
37	937	76.6	214	3	US-09-097-309-2	Sequence 2, Appl1
38	937	76.6	214	3	US-09-097-309-2	Sequence 2, Appl1
39	937	76.6	214	3	US-09-460-587-2	Sequence 2, Appl1
40	937	76.6	214	5	PCR-US93-07832-40	Sequence 40, Appl
41	937	76.6	227	3	US-09-097-309-6	Sequence 6, Appl1
42	937	76.6	237	3	US-09-097-171A-10	Sequence 10, Appl
43	937	76.6	237	3	US-09-422-712B-2	Sequence 2, Appl1
44	937	76.6	237	3	US-09-607-756-2	Sequence 2, Appl1
45	937	76.6	237	4	US-09-460-587-6	Sequence 6, Appl1

## ALIGNMENTS

RESULT 1  
US-09-049-672A-6  
Sequence 6, Application US/09049672A  
Patent No. 6135941  
GENERAL INFORMATION:  
APPLICANT: Hillman, Jennifer L.  
APPLICANT: Lal, Preeti  
APPLICANT: Tang, Y. Tom  
APPLICANT: Yue, Henry  
APPLICANT: Au-Young, Janice  
APPLICANT: Corley, Neil C.  
APPLICANT: Guegler, Karl J.  
APPLICANT: Baughn, Mariah R.  
TITLE OR INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/049, 672A  
FILING DATE: HERewith  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Cerrone, Michael C  
REGISTRATION NUMBER: 39,132  
REFERENCE/DOCKET NUMBER: PF-0497 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-855-0555  
TELEFAX: 650-845-4166  
TELEX:  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 234 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: COLSUCT01

CLONE: 2280869  
US-09-049-672A-6

Query Match 86.3%; Score 1056; DB 3; Length 234;  
Best Local Similarity 85.9%; Pred. No. 7,6e-79;  
Matches 201; Conservative 14; Mismatches 19; Indels 0; Gaps 0;

QY 1 MEAPQALLFLLLMLPDTTGEIVLTQSPATLSLSPGERATLACRASQTSRYLAWYQOKP 60  
DB 1 MEAPQALLFLLLMLPDSFGEIVMTQSPALVSLSPGERATLSCRASQSIGSIYAWYQOKP 60  
QY 61 GOAPRLLYDTSNRTATGIPARFSGSGSTDTLTSLSSLEPEDFAYVYCOQRFNMPWTGQ 120  
DB 61 GQSPRLLYGASTRATGVPPRFSGSGSTDEFTLTSLSSQSDPEDFALYYCOQYKGMPLTFGQ 120  
QY 121 GTRVEKRTVAAPSVFIFPPSDEQLKSGTASVYCLNNFYPREAKVQMKVDNALQSGNSQ 180  
DB 121 GTRVQIKRTVAAPSVFIFPPSDEQLKSGTASVYCLNNFYPREAKVQMKVDNALQSGNSQ 180  
QY 181 ESYTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 234  
DB 181 ESYTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 234

RESULT 2  
US-09-740-002-24  
Sequence 24, Application US/09740002  
Patent No. 6537809

GENERAL INFORMATION:  
APPLICANT: BRAMS, PETER  
APPLICANT: MORROW, PHILLIP  
TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN MONOCLONAL ANTIBODIES  
TITLE OF INVENTION: SPECIFIC TO RSV F-PROTEIN AND METHODS FOR THEIR  
FILE REFERENCE: 037003-0275759  
CURRENT APPLICATION NUMBER: US/09/740,002  
CURRENT FILING DATE: 2000-12-20  
PRIOR APPLICATION NUMBER: 09/335,697  
PRIOR FILING DATE: 1999-06-18  
PRIOR APPLICATION NUMBER: 08/488,376  
PRIOR FILING DATE: 1995-06-07  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 24  
LENGTH: 234  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-740-002-24

Query Match 81.2%; Score 993; DB 4; Length 234;  
Best Local Similarity 80.8%; Pred. No. 1e-73;  
Matches 189; Conservative 16; Mismatches 29; Indels 0; Gaps 0;

QY 1 MEAPQALLFLLLMLPDTTGEIVLTQSPATLSLSPGERATLACRASQTSRYLAWYQOKP 60  
DB 1 MEAPQALLFLLLMLRKARCDIOMTQSPSSLSASVGRVITTCRAGRASVYLMWYQHKP 60  
QY 61 GOAPRLLYDTSNRTATGIPARFSGSGSTDTLTSLSSLEPEDFAYVYCOQRFNMPWTGQ 120  
DB 61 GKAPRLLYAGSNLHRRVPSRFSGSGSTDTLTSLSSLEPEDFAYVYCOQAFSTPWTGQ 120  
QY 121 GTRVEKRTVAAPSVFIFPPSDEQLKSGTASVYCLNNFYPREAKVQMKVDNALQSGNSQ 180  
DB 121 GTRVEKRTVAAPSVFIFPPSDEQLKSGTASVYCLNNFYPREAKVQMKVDNALQSGNSQ 180  
QY 181 ESYTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 234  
DB 181 ESYTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 234

RESULT 3  
US-09-301-593-36  
Sequence 36, Application US/09301593A

Patent No. 6455677  
GENERAL INFORMATION:  
APPLICANT: Park, John E.  
APPLICANT: Garin-Chesa, Pilar  
APPLICANT: Bamberger, Uwe  
APPLICANT: Leger, Olivier  
APPLICANT: Saldanha, Jose W.  
APPLICANT: Retlig, Wolfgang J.  
TITLE OF INVENTION: PAP-specific Antibody with Improved Productibility  
FILE REFERENCE: 0652,1890001  
CURRENT APPLICATION NUMBER: US/09/301,593A  
CURRENT FILING DATE: 1999-04-29  
EARLIER APPLICATION NUMBER: EP 98107925.4  
EARLIER FILING DATE: 1998-04-30  
EARLIER APPLICATION NUMBER: US 60/086,049  
EARLIER FILING DATE: 1998-05-18  
NUMBER OF SEQ ID NOS: 108  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 36  
LENGTH: 240  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-301-593-36

Query Match 80.3%; Score 982; DB 4; Length 240;  
Best Local Similarity 78.8%; Pred. No. 8.4e-73;  
Matches 189; Conservative 22; Mismatches 23; Indels 6; Gaps 1;

QY 1 MEAPQALLFLLLMLPDTTGEIVLTQSPATLSLSPGERATLACRASQTSRYLAWYQOKP 60  
DB 1 MEAPQALLFLLLMLPDSFGEIVMTQSPALVSLSPGERATLSCRASQSIGSIYAWYQOKP 60  
QY 55 WYQOKPGQAPRLLYDTSNRTATGIPARFSGSGSTDTLTSLSSLEPEDFAYVYCOQRFNMP 114  
DB 61 WYQOKPGQAPRLLYDTSNRTATGIPARFSGSGSTDTLTSLSSLEPEDFAYVYCOQRFNMP 120  
QY 115 PWTGQGTVEKRTVAAPSVFIFPPSDEQLKSGTASVYCLNNFYPREAKVQMKVDNAL 174  
DB 121 PLTFGQGTVEKRTVAAPSVFIFPPSDEQLKSGTASVYCLNNFYPREAKVQMKVDNAL 180  
QY 175 QSGNSQSEVTRQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 234  
DB 181 QSGNSQSEVTRQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 240

RESULT 4  
US-08-276-852-153  
Sequence 153, Application US/08276852  
Patent No. 5652138  
GENERAL INFORMATION:  
APPLICANT: Burton, Dennis R  
APPLICANT: Barbas, Carlos F  
APPLICANT: Lerner, Richard A  
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS  
NUMBER OF SEQUENCES: 170  
CORRESPONDENCE ADDRESS:  
ADDRESS: The Scripps Research Institute, Office of  
ADDRESS: Patent Counsel  
STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,  
STREET: Mail Drop TPC8  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/276,852  
FILING DATE: 18-JUL-1994



```

: APPLICATION NUMBER: US 08/276,852
: FILING DATE: 18-JUL-1994
: APPLICATION NUMBER: US 08/178,302
: FILING DATE: 30-SEP-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/954,148
: FILING DATE: 30-SEP-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: Fitting, Thomas
: REGISTRATION NUMBER: 34,163
: REFERENCE/DOCKET NUMBER: SCRI452P
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 619-554-2937
: TELEFAX: 619-554-6312
: INFORMATION FOR SEQ ID NO: 153:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 235 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-899-575-153

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Query Match	80.0%	Score	978.5	DB 1	Length	235			
Best Local Similarity	82.1%	Pred. No.	1.6e-72						
Matches	193	Conservative	14	Mismatches	27	Indels	1	Gaps	1
QY	1	MEADQALLFLLLMLPDTGEIVLTQSPATLSLSPGERATLACRASQT-ASRYILAMYQOK	59						
Db	1	MGVPTQVLGLLMLLTDPARCEIVLTQSGTSLSLSGEATFSCRSRSHIRSRHVAWYGHK	60						
QY	60	PGCAQPLLIDYDTSNRATGIPARFGSGSGCTFTLSTLSLEPFDPVYVYCCQQRFNMPWFG	119						
Db	61	PGCAQPLRVITHVSNRRASGISDRFGSGSGCTDFTLITRVEEDDFALTYICQVYGASSYVFG	120						
QY	120	QGTVEEKRTVAADSVFLFPPSDQLASGTASVYCLNNFYPRKAYQWMDNALQSGNS	179						
Db	121	QGTLEKRRKTVAPASVFLFPPSDQLKSGTASVYCLNNFYPRKAYQWMDNALQSGNS	180						
QY	180	QESTTEDSDSDSTSLSTLTLKADYKHKHVVACEVTHQGLSSPYTSSFNREGC	234						
Db	181	QESTTEDSDSDSTSLSTLTLKADYKHKHVVACEVTHQGLSSPYTSSFNREGC	235						

```

; RESULT 7
PCT-US95-08743-153
; Sequence 153, Application PC/TUS9508743
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08743
FILING DATE: 11-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
INFORMATION FOR SEQ ID NO: 153:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
CCT-US95-08743-153

```

Query Match	80.0%	Score	978.5	DB	5	Length	235
Best Local Similarity	82.1%	Pred. NO.	1.6e-72				
Matches	193	Conservative	14	Mismatches	27	Indels	1
						Gaps	1

```

QY  MEMPADLLELLMLPDTGTGEVLQSPATLSPGGEATLACASOT -ASRLAWYQOK 59
    | : : | | | | | | | | | | | | | | | | | | | | : | : | : | | | |
Db  1 MGVPYOVLELLMLLTDARCELYLTQSGTSLSPGBERATPSCSSHSISIRRYAYQK 60

QY  60 PGQAPRLLYDTPSNRATGIPARFSGSGSGTDFTLSSLEPEDFNAVYYCOQRFNMPWTCG 119
    | | | | | : | | | | | | | | | | | | | | | | | | | | | | | |
    | | | | | : | | | | | | | | | | | | | | | | | | | | | | | |
Db  61 PGQAPRLVIGHVSNRASIGSDRFSSGSGTDFTLITRVEDEDFALVYCYQVYGAASYTCG 120

QY  120 QGTKEVEKRTVAAPSVFIFPPSDEQDKSGTASVYCLINFFPRGAKYQMKVYDNALSGNS 179
    | | | | | : | | | | | | | | | | | | | | | | | | | | | | | |
    | | | | | : | | | | | | | | | | | | | | | | | | | | | | | |
Db  121 QGKLEKERTVAAPSVFIFPPSDEQDKSGTASVYCLINFFPRGAKYQMKVYDNALSGNS 180

QY  180 QESVTEBODSKDSTYLSLSFTLSKADYEKHHVYACEYTHQGLSPVTKSFNRGEC 234
    | | | | | : | | | | | | | | | | | | | | | | | | | | | | | |
Db  181 QESVTEBODSKDSTYLSLSFTLSKADYEKHHVYACEYTHQGLSPVTKSFNRGEC 235

```

```

: RESULT 8
: US-08-812-586-16
: Sequence 16, Application US/08812586
: Patent No. 6048704
:
: GENERAL INFORMATION:
: APPLICANT: Martin David Tilson
: TITLE OF INVENTION: PURIFIED AND RECOMBINANT ANTIGENIC
: TITLE OF INVENTION: PROTEINS ASSOCIATED WITH ABDOMINAL AORTIC ANEURYSM (AAA)
: TITLE OF INVENTION: DISEASE, AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF
: NUMBER OF SEQUENCES: 61
:
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Cooper & Dunham LLP
: STREET: 1185 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: U.S.A.
: ZIP: 10036
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/812,586
: FILING DATE: 07-MAR-1997
: CLASSIFICATION: A35
:
: ATTORNEY/AGENT INFORMATION:
: NAME: White, John P.
: REGISTRATION NUMBER: 28,678
: REFERENCE/DOCKET NUMBER: 0575/53862-A
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 278-0400
: TELEFAX: (212) 391-0525
:
: INFORMATION FOR SEQ ID NO: 16:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 235 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
:
: MOLECULE TYPE: protein
:
: US-08-812-586-16

```

[illegible]

Db 123 GTKVEIKRTVAAPSVFIPPSPDEQLKSGTASVGLNNFYPREAKVQWMDNALQSGNSQ 182  
181 ESVTEDSKDSTYSLSSTITLTKADYEKKVYACEYTHOGLSSPVTKSFNRGE 233  
Db 183 ESVTEDSKDSTYSLSSTITLTKADYEKKVYAGEVTHOGLSSPVTKSFNRGE 235

## RESULT 9

US-09-535-832A-17  
Sequence 17, Application US/09535832A  
Patent No. 6537769  
GENERAL INFORMATION:  
APPLICANT: Tilson, Martin David  
TITLE OF INVENTION: Purified and Recombinant Antigenic Proteins Associated  
TITLE OF INVENTION: with Abdominal Aortic Aneurysm (AAA) Disease, and  
TITLE OF INVENTION: Diagnostic and Therapeutic use thereof  
FILE REFERENCE: 53862-A2  
CURRENT APPLICATION NUMBER: US/09/535,832A  
CURRENT FILING DATE: 2000-03-28  
NUMBER OF SEQ ID NOS: 57  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 17  
LENGTH: 235  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-535-832A-17

Query Match 80.0%; Score 978; DB 4; Length 235;  
Best Local Similarity 84.1%; Pred. No. 1.7e-72;  
Matches 196; Conservative 8; Mismatches 29; Indels 0; Gaps 0;

QY 1 MEAPQDLLELLMLPDTTGEIYLVQSPATLSLSPERATLACRAQTASRIYLAQQR 60  
Db 3 MRPVQDLGLLLMLPGACAIRIAQSPSLASTDRTVITCRASQISNTLAWYQQR 62  
QY 61 GOAPRLIYDTSNRATGIPARFSGSGTDFTLSSLEPEDFAVYCCOORENMPWTFQ 120  
Db 63 GQAPRLIYDASSRATGIDRFSGSGGTDFTLISLEPEDFAVYGGQYGSPLTFQ 122  
QY 121 GTRVEKRTVAAPSVFIPPSPDEQLKSGTASVGLNNFYPREAKVQWMDNALQSGNSQ 180  
Db 123 GTRVEIKRTVAAPSVFIPPSPDEQLKSGTASVGLNNFYPREAKVQWMDNALQSGNSQ 182  
QY 181 ESVTEDSKDSTYSLSSTITLTKADYEKKVYACEYTHOGLSSPVTKSFNRGE 233  
Db 183 ESVTEDSKDSTYSLSSTITLTKADYEKKVYAGEVTHOGLSSPVTKSFNRGE 235

## RESULT 10

US-07-916-098A-56  
Sequence 56, Application US/07916098A  
Patent No. 5871732  
GENERAL INFORMATION:  
APPLICANT: BURKILY, LINDA C.  
APPLICANT: THOMAS, DAVID W.  
APPLICANT: ROSA, MARGARET D.  
APPLICANT: ROSA, JOSEPH J.  
TITLE OF INVENTION: ANTI-CD4 ANTIBODY HOMOLOGS USEFUL IN  
TITLE OF INVENTION: PROPHYLAXIS AND TREATMENT OF AIDS, AHC AND HIV INFECTION  
NUMBER OF SEQUENCES: 61  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ALLEGRETTI & WITCOFF, LTD.  
STREET: 10 SOUTH WACKER DRIVE  
CITY: CHICAGO  
STATE: ILLINOIS  
COUNTRY: U.S.A.  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WORD PERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/916,098A  
FILING DATE: July 24, 1992  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US91/08843  
FILING DATE: No. 5871732ember 27, 1991  
CLASSIFICATION: 424  
APPLICATION NUMBER: 07/618,542  
FILING DATE: No. 5871732ember 27, 1990  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: JOHN J. MC DONNELL  
REGISTRATION NUMBER: 26,949  
REFERENCE/DOCKET NUMBER: 92,310-G  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 715-1000  
TELEFAX: (312) 715-1234  
TELEX: 910/221-5317  
INFORMATION FOR SEQ ID NO: 56:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 241 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-916-098A-56

Query Match 79.4%; Score 970.5; DB 2; Length 241;  
Best Local Similarity 79.2%; Pred. No. 7.3e-72;  
Matches 190; Conservative 18; Mismatches 25; Indels 7; Gaps 2;

QY 1 MEAPQDLLELLMLPDTTGEIYLVQSPATLSLSPERATLACRA-----SQTASRIYA 54  
Db 3 MRPVQDLGLLLMLPGACAIRIAQSPSLASTDRTVITCRASQISNTLAWYQQR 62  
QY 55 WYQKRGQAPRLIYDTSNRATGIPARFSGSGTDFTLSSLEPEDFAVYCCOORENMPWTFQ 114  
Db 63 WYQKRGQAPRLIYDTSNRATGIPARFSGSGTDFTLSSLEPEDFAVYCCOORENMPWTFQ 112  
QY 115 PWTGGTKEVFEKRTVAAPSVFIPPSPDEQLKSGTASVGLNNFYPREAKVQWMDNAL 174  
Db 123 R-TFGGTKEVFEKRTVAAPSVFIPPSPDEQLKSGTASVGLNNFYPREAKVQWMDNAL 181  
QY 175 QSGNSEVTEODSKDSTYSLSSTITLTKADYEKKVYACEVTHOGLSSPVTKSFNRGE 234  
Db 182 QSGNSEVTEODSKDSTYSLSSTITLTKADYEKKVYAGEVTHOGLSSPVTKSFNRGE 241

## RESULT 11

US-08-480-753-6  
Sequence 6, Application US/08480753  
Patent No. 5830675  
GENERAL INFORMATION:  
APPLICANT: Targan M.D., Stephan R.  
APPLICANT: Vardich Ph.D., Aida M.  
TITLE OF INVENTION: METHODS FOR SELECTIVELY DETECTING  
TITLE OF INVENTION: PERINUCLEAR ANTI-NEUTROPHIL CYTOPLASMIC ANTIBODY OF  
TITLE OF INVENTION: ULCERATIVE COLITIS, PRIMARY SCLEROSING CHOLANGITIS, OR  
TITLE OF INVENTION: TYPE I AUTOIMMUNE HEPATITIS  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wendy A. Whiteford, Esq.  
STREET: 444 South Flower Street, Suite 2000  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25

TOPOLOGY: Linear ;

RESULT 13  
 US-08-837-058-11  
 Sequence 11, Application US/08837058  
 Patent No. 6074835  
 GENERAL INFORMATION:  
 APPLICANT: Braun, Jonathan  
 APPLICANT: Targan, Stephan R.  
 APPLICANT: Eggena, Mark  
 TITLE OF INVENTION: Diagnosis, Prevention and Treatment of  
 TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using  
 TITLE OF INVENTION: Histone H1  
 NUMBER OF SEQUENCES: 26  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Campbell & Flores LLP  
 STREET: 4370 La Jolla Village Drive, Suite 700  
 CITY: San Diego  
 STATE: California  
 COUNTRY: USA  
 ZIP: 92122  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/837,058  
 FILING DATE:  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Campbell, Cathryn A.  
 REGISTRATION NUMBER: 31,815  
 REFERENCE/DOCKET NUMBER: P-PM 2438  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (619) 535-9001  
 TELEFAX: (619) 535-8949  
 INFORMATION FOR SEQ ID NO: 11:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 214 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear



```
MOLECULE TYPE: protein
US-08-837-058-11

Query Match      78.7%; Score 962.5; DB 3; Length 214;
Best Local Similarity 88.7%; Pred. No. 2.8e-71;
Matches 188; Conservative 5; Mismatches 18; Indels 1; Gaps 1;

QY 24 LTOSPATLSPGERATLACRASQTAAS-RYLAWYQOKPGQAPRLIYDTSNRATGIPARF 82
DB 3 LTOSGCTLSLFGGERATLSCRASQTRISTSFLLAWYQOKPGQAPRLIYDTSNRATGIPARF 62
QY 83 SSGSGTDFTLTISLSEPEDEFAVYCCQGRFNMPTFGQGTVEKRYVAAPSVFTFPPSD 142
DB 63 SASWSGTDFTLTISLSEPEDEFAVYCCQHYGSGSPMTFGQGTVEIKRTVAAPSVFTFPPSD 122
QY 143 EQLKSGTASVYCLLNFFPREAKYQWKVDNALQSGNSQSESYEDQSKDSTYSLSTLTLS 202
DB 123 EQLKSGTASVYCLLNFFPREAKYQWKVDNALQSGNSQSESYEDQSKDSTYSLSTLTLS 182
QY 203 KADYEKHKYACEVTHQGLSSPVTKSFNRGEC 234
DB 183 KADYEKHKYACEVTHQGLSSPVTKSFNRGEC 214

RESULT 14
US-09-417-264-11
Sequence 11, Application US/09417264
Patent No. 6537768
GENERAL INFORMATION:
APPLICANT: Braun, Jonathan
APPLICANT: Chavay, Offer
TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/417,264
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/041,889
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-417-264-11

Query Match      78.7%; Score 962.5; DB 4; Length 214;
Best Local Similarity 88.7%; Pred. No. 2.8e-71;
Matches 188; Conservative 5; Mismatches 18; Indels 1; Gaps 1;
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QY 24 LTOSPATLSPGERATLACRASQTAAS-RYLAWYQOKPGQAPRLIYDTSNRATGIPARF 82
DB 3 LTOSGCTLSLFGGERATLSCRASQTRISTSFLLAWYQOKPGQAPRLIYDTSNRATGIPARF 62
QY 83 SSGSGTDFTLTISLSEPEDEFAVYCCQGRFNMPTFGQGTVEKRYVAAPSVFTFPPSD 142
DB 63 SASWSGTDFTLTISLSEPEDEFAVYCCQHYGSGSPMTFGQGTVEIKRTVAAPSVFTFPPSD 122
QY 143 EQLKSGTASVYCLLNFFPREAKYQWKVDNALQSGNSQSESYEDQSKDSTYSLSTLTLS 202
DB 123 EQLKSGTASVYCLLNFFPREAKYQWKVDNALQSGNSQSESYEDQSKDSTYSLSTLTLS 182
QY 203 KADYEKHKYACEVTHQGLSSPVTKSFNRGEC 234
DB 183 KADYEKHKYACEVTHQGLSSPVTKSFNRGEC 214

RESULT 15
US-09-315-926A-79
Sequence 79, Application US/09315926A
Patent No. 6498027
GENERAL INFORMATION:
APPLICANT: Es van, Helmut
APPLICANT: Havenga, Menzo
APPLICANT: Verlinden, Stefan
TITLE OF INVENTION: TARGETED DELIVERY THROUGH A CATIONIC AMINO ACID TRANSPORTER
FILE REFERENCE: 2183-4080US
CURRENT FILING DATE: US/09/315,926A
PRIOR FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: EP 99201593.3
PRIOR FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: EP 98201693.3
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 81
SOFTWARE: PatentIn version 3.0
SEQ ID NO 79
LENGTH: 236
TYPE: PR
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Description of Artificial Sequence: phage
NAME/KEY: PEPTIDE
LOCATION: (1)..(236)
OTHER INFORMATION: /note="hCAT1 amino acid sequence"
US-09-315-926A-79

Query Match      78.7%; Score 962.5; DB 4; Length 236;
Best Local Similarity 82.9%; Pred. No. 3.2e-71;
Matches 194; Conservative 11; Mismatches 24; Indels 5; Gaps 3;

QY 6 QLLFLLMLP---DTGEIVLTOSPATLSPGERATLACRASQTAASRYLAWYQOKPG 61
DB 3 KLLFALPLVLPFYPSHALETTLTOSGCTLSLPGACATLSCRASQSVSSRNLAAMYQOKPG 62
QY 62 QAPRLIYDTSNRATGIPARFSGSGSGTDFTLTISLSEPEDEFAVYCCQGRFNMPTFGQGT 121
DB 63 QAPRLIYDTSNRATGIPARFSGSGSGTDFTLTISLSEPEDEFAVYCCQGRFNMPTFGQGT 122
QY 122 TKVEFKR-TVAAPSVFTFPPSDQQLKSGTASVYCLLNFFPREAKYQWKVDNALQSGNSQ 180
DB 123 TKVEIKRGTVAAPSVFTFPPSDQQLKSGTASVYCLLNFFPREAKYQWKVDNALQSGNSQ 182
QY 181 ESYTQDSKSTYSLSTLTLSKADYEKHKYACEVTHQGLSSPVTKSFNRGEC 234
DB 183 ESYTQDSKSTYSLSTLTLSKADYEKHKYACEVTHQGLSSPVTKSFNRGEC 236

Search completed: September 12, 2003, 13:05:15
Job time : 15.2203 secs
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Db 61 GOSPELVITYGASSRASGVAPRSGSGCTEFTLTLSIQSEFPAYVYCOQYKMKPHTEGQ 120  
Oy 121 GTKVEFRKTVAAPSVFIFPPSDEOLKSGTASVYCLNNFYPREAKVQKVDNALQSGMSQ 180  
Db 121 GTKLDIKRTVAAPSVFIFPPSDEOLKSGTASVYCLNNFYPREAKVQKVDNALQSGMSQ 180  
Oy 181 ESYTEQDSKSDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 234  
Db 181 ESYTEQDSKSDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 234

## RESULT 2

08NEKO PRELIMINARY: PRT: 239 AA.  
AC 08NEKO;  
DT 01-OCT-2002 (TREMBLrel. 22, Created)  
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)  
DE 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
OS Hypothetical protein.  
OC Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Prostate;  
RA Strausberg R.;  
RL Submitted (JUN-2002) to the EMBL/Genbank/DBJ databases.  
DR EMBL: BC030814; AA030814.1; -  
DR InterPro: IPR007110; Iq-like.  
DR InterPro: IPR003597; Iq-cl.  
DR InterPro: IPR003006; Iq\_MHC.  
DR InterPro: IPR003596; Iq-V.  
DR Pfam: PF00047; Iq; 2.  
DR SMART: SM00407; Iqcl; 1.  
DR SMART: SM00406; IGV; 1.  
DR PROSITE: PS50835; Iq-LIKE; 2.  
DR PROSITE: PS00290; Iq\_MHC; 1.  
DR Hypothetical protein.  
KW Hypothetical protein.  
SQ SEQUENCE 239 AA; 26024 MW; F5E20AD3B0552C0A CRC64;

Query Match 78.6%; Score 961.5; DB 4; Length 239;  
Best Local Similarity 77.4%; Pred. No. 9.1e-84;  
Matches 185; Conservative 20; Mismatches 29; Indels 5; Gaps 1;

Oy 1 MEAPQQLFLLMLPDTTGEIVLTQSPATLSLSPGERATLACRASQT-----ASRYLAW 55  
Db 1 MRLPAQLGLMLMWSSGSDIVMTQSPVTPTEGEPASISCRSSQSLHSDGNYLDM 60  
Oy 56 YQKPGQAPRLIIYDTSNRATGIPARFSGSGGTDFTLISLSEPEDFAVYVCOQRFNMP 115  
Db 61 YLQKQGSPQLLIYGSNRRASGVPDRFSGSGGTDFTLIKISKEADVDGIYCMQGLQTP 120  
Oy 116 WFGGQTVKFRKRVAAAPSVFIFPPSDEOLKSGTASVYCLNNFYPREAKVQKVDNALQ 175  
Db 121 QTFGGGTVEIKRTVAAPSVFIFPPSDEOLKSGTASVYCLNNFYPREAKVQKVDNALQ 180  
Oy 176 SGNSESVTEQDSKSDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 234  
Db 181 SGNSESVTEQDSKSDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 239

## RESULT 3

08TCDO PRELIMINARY: PRT: 239 AA.  
AC 08TCDO;  
DT 01-JUN-2002 (TREMBLrel. 21, Created)  
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)  
DE 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
OS Hypothetical protein.  
OC Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RA Strausberg R.;  
RL Submitted (FEB-2002) to the EMBL/Genbank/DBJ databases.  
DR EMBL: BC022362; AA022362.1; -  
DR InterPro: IPR007110; Iq-like.  
DR InterPro: IPR003006; Iq\_MHC.  
DR InterPro: IPR003596; Iq-V.  
DR Pfam: PF00047; Iq; 2.  
DR SMART: SM00406; IGV; 1.  
DR PROSITE: PS50835; Iq-LIKE; 2.  
DR PROSITE: PS00290; Iq\_MHC; 1.  
DR Hypothetical protein.  
KW Hypothetical protein.  
SQ SEQUENCE 239 AA; 26234 MW; F4CEDC3A3B03871D CRC64;

Query Match 78.2%; Score 956.5; DB 4; Length 239;  
Best Local Similarity 75.3%; Pred. No. 2.7e-83;  
Matches 180; Conservative 28; Mismatches 26; Indels 5; Gaps 1;

Oy 1 MEAPQQLFLLMLPDTTGEIVLTQSPATLSLSPGERATLACRASQT-----ASRYLAW 55  
Db 1 MRLPAQLGLMLMWSSGSDIVMTQSPVTPTEGEPASISCRSSQSLHSDGNYLDM 60  
Oy 56 YQKPGQAPRLIIYDTSNRATGIPARFSGSGGTDFTLISLSEPEDFAVYVCOQRFNMP 115  
Db 61 FQKRGQSPRLIIYVSNRDSGVPDRFSGSGGTDFTLIKRIVEADVGVCQMGTHMP 120  
Oy 116 WFGGQTVKFRKRVAAAPSVFIFPPSDEOLKSGTASVYCLNNFYPREAKVQKVDNALQ 175  
Db 121 STFGGQTKLEIKRTVAAPSVFIFPPSDEOLKSGTASVYCLNNFYPREAKVQKVDNALQ 180  
Oy 176 SGNSESVTEQDSKSDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 234  
Db 181 SGNSESVTEQDSKSDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 239

## RESULT 4

099M37 PRELIMINARY: PRT: 238 AA.  
AC 099M37;  
DT 01-JUN-2001 (TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
DE 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_Taxid=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC Strausberg R.;  
RL Submitted (JAN-2001) to the EMBL/Genbank/DBJ databases.  
DR EMBL: BC002035; AA02035.1; -  
DR HSP: P01679; 2PBJ.  
DR InterPro: IPR007110; Iq-like.  
DR InterPro: IPR003006; Iq\_MHC.  
DR InterPro: IPR003596; Iq-V.  
DR Pfam: PF00047; Iq; 2.  
DR SMART: SM00406; IGV; 1.  
DR PROSITE: PS50835; Iq-LIKE; 2.  
DR PROSITE: PS00290; Iq\_MHC; 1.  
DR Hypothetical protein.  
KW Hypothetical protein.  
SQ SEQUENCE 238 AA; 26344 MW; FB2B06A0B801330A CRC64;

Query Match 59.6%; Score 729; DB 11; Length 238;  
Best Local Similarity 56.5%; Pred. No. 1.5e-61;  
Matches 135; Conservative 44; Mismatches 54; Indels 6; Gaps 2;

Oy 1 MEAPQQLFLLMLPDTTGEIVLTQSPATLSLSPGERATLACRASQT-----ASRYLAW 55  
Db 1 MRLPAQLGLMLMWSSGSDIVMTQSPVTPTEGEPASISCRSSQSLHSDGNYLDM 60



```

Db      61 DGTVLLIYSSLSHSGVPSRPSGSGSHVSLTSLNLEPEDIAIYCOQYQSQFPFTGGS 120
      121 GTKVEFKRTVAAPSVFIFPPSDEOLKSGTASVCLINNFYPREAIVQKVNALQSGNSQ 180
      121 GTKLEIKRADAPYTSIFPPSSEQLTSGCASYVCLINNFYRKDIIVKKIKIDSEKQNGVL 180
Qy      181 ESYTEQDSKDSYSLSTLTLSKADYEKHKVYACEVTHQGLSSPYTKSFNRGEC 234
      1 ESYTEQDSKDSYSLSTLTLTLDKDEYERHNSYTCATHTKSTSPYVKSFRNREC 234
Db      181 NSMTQDSKDSYSSMSSTLTTLTKDEYERHNSYTCATHTKSTSPYVKSFRNREC 234

```

## RESULT 8

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Q8K0F8 PRELIMINARY: PRT; 239 AA.
AC Q8K0F8;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Breast tumor;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL; BC031498; AAH31498.1;
DR InterPro; IPR002198; ADH_short.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00409; Ig_2.
DR SMART; SM00407; Ig_c1.
DR SMART; SM00406; Ig_v.
DR PROSITE; PS00061; ADH_SHORT; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 2636 MW; D7BE84398AA341F0 CRC64;

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Query Match      57.4%; Score 702.5; DB 11; Length 239;
Best Local Similarity 55.2%; Pred. No. 5,2e-59;
Matches 132; Conservative 43; Mismatches 59; Indels 5; Gaps 1;

Qy      1 MEAPQQLFLLLMLPDTTGEIVLTQSPATLSLSPGERATLACRASQT-----ASRYLAW 55
      1 MEAPQQLFLLLMLPDTTGEIVLTQSPATLSLSPGERATLACRASQT-----ASRYLAW 55
Db      1 MMSPAQFLFLVLVLSIOEINGDVMTQPTLTSLTIGQPASISCKSSQSLFYTNCKMYLSM 60
      1 MMSPAQFLFLVLVLSIOEINGDVMTQPTLTSLTIGQPASISCKSSQSLFYTNCKMYLSM 60
Qy      56 YQKRGQAPRLIYDTSNRATGIPARFSGSGSGTDFTLSTLSLEPEDFAVYVCOQRFNMP 115
      56 YQKRGQAPRLIYDTSNRATGIPARFSGSGSGTDFTLSTLSLEPEDFAVYVCOQRFNMP 115
Db      61 LLQRFQGPCKRLISLVSKLDSGVPDRFSGSGSDFTLTLSKIVEAEDLGVYICLOSTHFP 120
      61 LLQRFQGPCKRLISLVSKLDSGVPDRFSGSGSDFTLTLSKIVEAEDLGVYICLOSTHFP 120
Qy      116 WTFGGGTVEFKRTVAAPSVFIFPPSDEOLKSGTASVCLINNFYPREAIVQKVNALQ 175
      116 WTFGGGTVEFKRTVAAPSVFIFPPSDEOLKSGTASVCLINNFYPREAIVQKVNALQ 175
Db      121 YTFGGGTVEFKRTVAAPSVFIFPPSDEOLKSGTASVCLINNFYRKDIIVKKIKIDSEK 180
      121 YTFGGGTVEFKRTVAAPSVFIFPPSDEOLKSGTASVCLINNFYRKDIIVKKIKIDSEK 180
Qy      176 SGNSQESYTEDSKDSYSLSTLTLSKADYEKHKVYACEVTHQGLSSPYTKSFNRGEC 234
      176 SGNSQESYTEDSKDSYSLSTLTLSKADYEKHKVYACEVTHQGLSSPYTKSFNRGEC 234
Db      181 QNGVLNSWTQDSKDSYSSMSSTLTTLTKDEYERHNSYTCATHTKSTSPYVKSFRNREC 239
      181 QNGVLNSWTQDSKDSYSSMSSTLTTLTKDEYERHNSYTCATHTKSTSPYVKSFRNREC 239

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## RESULT 9

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Q91WF8 PRELIMINARY: PRT; 234 AA.
AC Q91WF8;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Hypothetical 23.9 kDa protein.

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OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Colon;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; BC015292; AAH15292.1;
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR InterPro; IPR001865; Ribosomal_S2.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00406; Ig_v.
DR PROSITE; PS00290; IG_MHC; 1.
DR PROSITE; PS00962; RIBOSOMAL_S2_1; 1.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25929 MW; B0D0B0E6EB7812D2 CRC64;

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Query Match 57.3%; Score 701; DB 11; Length 234;

Best Local Similarity 58.1%; Pred. No. 7,1e-59;

Matches 136; Conservative 34; Mismatches 64; Indels 0; Gaps 0;

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Qy      1 MEAPQQLFLLLMLPDTTGEIVLTQSPATLSLSPGERATLACRASQTSRYLAWYQKP 60
      1 MEAPQQLFLLLMLPDTTGEIVLTQSPATLSLSPGERATLACRASQTSRYLAWYQKP 60
Db      1 MMSPAQFLGLLCLFCQGRCDIQMTQTSLSASLGDVITISCRASQDISVNLWYQKP 60
      1 MMSPAQFLGLLCLFCQGRCDIQMTQTSLSASLGDVITISCRASQDISVNLWYQKP 60
Qy      61 GQAPRLIYDTSNRATGIPARFSGSGSGTDFTLSTLSLEPEDFAVYVCOQRFNMPWTGQ 120
      61 GQAPRLIYDTSNRATGIPARFSGSGSGTDFTLSTLSLEPEDFAVYVCOQRFNMPWTGQ 120
Db      61 DGTVLLIYSSLSRLYLVPSRPSGSGSDTSLTSLNLEQBDIAIYFCQDQNTPEPFTGGS 120
      61 DGTVLLIYSSLSRLYLVPSRPSGSGSDTSLTSLNLEQBDIAIYFCQDQNTPEPFTGGS 120
Qy      121 GTKVEFKRTVAAPSVFIFPPSDEOLKSGTASVCLINNFYPREAIVQKVNALQSGNSQ 180
      121 GTKVEFKRTVAAPSVFIFPPSDEOLKSGTASVCLINNFYPREAIVQKVNALQSGNSQ 180
Db      121 GTKLEIKRADAPYTSIFPPSSEQLTSGCASYVCLINNFYRKDIIVKKIKIDSEKQNGVL 180
      121 GTKLEIKRADAPYTSIFPPSSEQLTSGCASYVCLINNFYRKDIIVKKIKIDSEKQNGVL 180
Qy      181 ESYTEQDSKDSYSLSTLTLSKADYEKHKVYACEVTHQGLSSPYTKSFNRGEC 234
      181 ESYTEQDSKDSYSLSTLTLSKADYEKHKVYACEVTHQGLSSPYTKSFNRGEC 234
Db      181 NSMTQDSKDSYSSMSSTLTTLTKDEYERHNSYTCATHTKSTSPYVKSFRNREC 234
      181 NSMTQDSKDSYSSMSSTLTTLTKDEYERHNSYTCATHTKSTSPYVKSFRNREC 234

```

## RESULT 10

```

Q8VC55 PRELIMINARY: PRT; 239 AA.
AC Q8VC55;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Hypothetical 26.3 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Colon;
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL; BC011781; AAH11781.1;
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00406; Ig_v.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 26303 MW; C16119CACAC25C373 CRC64;

```

Query Match 57.3%; Score 700.5; DB 11; Length 239;

Best Local Similarity 55.2%; Pred. No. 8,1e-59;

Matches 132; Conservative 43; Mismatches 59; Indels 5; Gaps 1;

```

Qy      1 MEAPQQLFLLLMLPDTTGEIVLTQSPATLSLSPGERATLACRASQT-----ASRYLAW 55
      1 MEAPQQLFLLLMLPDTTGEIVLTQSPATLSLSPGERATLACRASQT-----ASRYLAW 55

```

```
Db      1 MKLPVLLVLLFTSPASSSDVYLQTPLSLPVNIQDQASICKSTKSLNSDGFYTLDM 60
OY      56 YQKQPGQAPRLLIYDTSNATGIPARFSSGSGTDFTLSSLEPPDFAVYTCQGFNMP 115
Db      61 YLQKPGQSPOLLILYLVSNRFGVPPDFSSGSGTDFTLKSIRVEADLGVYCCFQSNHLP 120
OY      116 MPFGQGTKEFKRRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQMKVNALQ 175
Db      121 YTFGGGTKEIKRADAPATVSIFFPSSEDLTSGGASVCFLLNFFPKDINVKKKIDGSE 180
OY      176 SGNDSQSVTEQDSKDSSTYLSSTLLSKADYERKHVYACEVTHQGLSPVTKSFNREG 234
Db      181 QMGVLNSMTDQSKDSTYSMSSTLLTKDEYERHNSYTCGATHKSTSPIVKSFNNEC 239

RESULT 11
O91MS9  PRELIMINARY:      PRT:      233 AA.
AC      091MS9:
DT      01-DEC-2001 (TReMBLrel. 19, Created)
DT      01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DE      Hypothetical 25.8 kDa protein (Fragment).
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE-Colon;
RA      Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR      EMBL: BC013496; AAH13496.1; -.
DR      InterPro: IPR007110; Ig_Like.
DR      InterPro: IPR003006; Ig_MHC.
DR      InterPro: IPR003596; Ig_V.
DR      Pfam: PF00047; Ig_2.
DR      SMART: SM00406; IGV_1.
DR      PROSITE: PS50835; IG_Like; 2.
DR      PROSITE: PS00290; IG_MHC; 1.
KW      Hypothetical protein.
FT      NON_TER
SQ      SEQUENCE      233 AA; 25781 MW; B1C184DA149A16EB CRC64;

Query Match      56.4%; Score 690; DB 11; Length 233;
Best Local Similarity 58.0%; Pred. No. 7.9e-58;
Matches 130; Conservative 35; Mismatches 59; Indels 0; Gaps 0;

OY      11 LLLMLPDTGETVLQSPATLSLSPGERATLACRASOTASRYLAWYQKRGQAPRLIYD 70
Db      10 LLLCFQGSRCIDIQMTQTTSLSLASLGDRVYISCSGSGGIANVYLMYQKRPDGTVKLLIY 69
OY      71 TSNRATGIPARFSSGSGTDFTLSSLEPPDFAVYTCQGFNMPPTFGQGTKEFKRTV 130
Db      70 TSLHSGVPSRFGSSSGTDTYSLTISNLEPEDATYTCQGYRXLPTFGGGLLEIKRAD 129
OY      131 AAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQMKVNALQSGNSQSVTEQDSKD 190
Db      130 AAPVSIFFPSSSEQLTSGGASVCFLLNFFPKDINVKKKIDGSEONGVLNSMTDQSKD 189
OY      191 STYVSLSSTLLTSLKADYERKHVYACEVTHQGLSPVTKSFNREGC 234
Db      190 STYMSSTLLTKDEYERHNSYTCGATHKSTSPIVKSFNNEC 233

RESULT 12
O91W12  PRELIMINARY:      PRT:      235 AA.
AC      091W12:
DT      01-DEC-2001 (TReMBLrel. 19, Created)
DT      01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT      01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE      Unknown (Protein for MGC:6582).
```

```
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE-Breast tumor;
RA      Strausberg R.;
DR      Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR      EMBL: BC006643; AAH06643.1; -.
DR      InterPro: IPR007110; Ig_Like.
DR      InterPro: IPR003006; Ig_MHC.
DR      InterPro: IPR003596; Ig_V.
DR      Pfam: PF00047; Ig_2.
DR      SMART: SM00406; IGV_1.
DR      PROSITE: PS50835; IG_Like; 2.
DR      PROSITE: PS00290; IG_MHC; 1.
KW      Hypothetical protein.
FT      NON_TER
SQ      SEQUENCE      235 AA; 26021 MW; 5FC73BDEBD5E8FEF CRC64;

Query Match      55.3%; Score 676.5; DB 11; Length 235;
Best Local Similarity 59.5%; Pred. No. 1.6e-56;
Matches 128; Conservative 31; Mismatches 55; Indels 1; Gaps 1;

OY      20 GETVLQSPATLSLSPGERATLACRASOTASRYLAWYQKRGQAPRLIYDTSNATGIP 79
Db      22 GQIVLTQSPRAIMKASPERYTMTCASSSYS-HMHYQOK;GTSPPKRWITDTKLTSGVP 80
OY      80 ARFSGSGTDFTLSSLEPPDFAVYTCQGFNMPPTFGQGTKEFKRRTVAAPSVFIFP 139
Db      81 DRFGSGSGTYSSTLTISNLEPEDAVATYYCQWGRNPPTFG/GTKLEIKRADAPATVSIFF 140
OY      140 PSDEQLKSGTASVCLLNNFYPREAKVQMKVNALQSGNSQSVTEQDSKDSYLSSTLL 199
Db      141 PSSEQLTSGGASVCFLLNFFPKDINVKKKIDGSEONGV.JNSMTDQSKDSYMSSTL 200
OY      200 TLSKADYERKHVYACEVTHQGLSPVTKSFNREGC 234
Db      201 TLTKDEYERHNSYTCGATHKSTSPIVKSFNNEC 235

RESULT 13
O9RIAS  PRELIMINARY:      PRT:      214 AA.
AC      09RIAS:
DT      01-MAY-2000 (TReMBLrel. 13, Created)
DT      01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT      01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE      kappa light chain of Mab7 (Fragment).
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT      antibody (Mab 7, its light and heavy chains) and construction of a
RT      single chain antibody (scFv).";
DR      Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR      EMBL: AF152371; AAD4042.1; -.
DR      HSSP: P01679; 2FBJ.
DR      InterPro: IPR007110; Ig_Like.
DR      InterPro: IPR003006; Ig_MHC.
DR      InterPro: IPR003596; Ig_V.
DR      Pfam: PF00047; Ig_2.
DR      SMART: SM00406; IGV_1.
DR      PROSITE: PS50835; IG_Like; 2.
DR      PROSITE: PS00290; IG_MHC; 1.
KW      Hypothetical protein.
FT      NON_TER
SQ      SEQUENCE      214 AA; 23922 MW; 52BA205FDE95E2A CRC64;

Query Match      55.3%; Score 676; DB 11; Length 214;
```

Best Local Similarity 57.5%; Pred. No. 1.5e-56;  
Matches 123; Conservative 37; Mismatches 54; Indels 0; Gaps 0;

```
OY 21 EIVLTOSPATLSLSPGERATLACRASOTASRYLAWYQOQPGQAPRLIYDTSNRATGPA 80
DB 1 DIOLTOSSSWYASLGERVYITCKASQDINSTLSWFOOKPKSPPTLIYRANRLVDGPS 60
OY 81 RFSGSGCTDPTLSTLSLEPEDFAVYCCQRFNFWPTFGCTKVEFKRTVAAPSVFIIPP 140
DB 61 RFSGSGGQDYSLRTISLEYEDMGITYCLOQDEFFFTGSGTKLEIKRADAPTVSIFPP 120
OY 141 SDEOLKSGTASVCLNNFTYPREAKVQKVDNALQSGNSQSVTEYDQSKDSTYSLSSTLT 200
DB 121 SSEDLTSGGASVCFLLNFPKIDINVKWKIDGSEKONGVLSMTDQDSKSTYSMSSTLT 180
OY 201 LSKADYEKKHYACEVTHQGLSSPYTKSFNREGC 234
DB 181 LTKDEYERHNSITCEATHTKSTSPYVKCFNRNEC 214
```

## RESULT 14

O8R028 PRELIMINARY: PRT: 234 AA.

```
AC O8R028. 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Hypothetical 25.7 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Mammary gland;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC028540; AAH28540.1;
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00406; IGV_1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25702 MW; 148377F9C1CD0AEE CRC64;
```

Query Match 53.6%; Score 655; DB 11; Length 234;

Best Local Similarity 54.8%; Pred. No. 1.8e-54;  
Matches 126; Conservative 33; Mismatches 71; Indels 0; Gaps 0;

```
OY 5 AQLFLLLMLPDTGELVLTQSPATLSLSPGERATLACRASOTASRYLAWYQOQPGQAP 64
DB 5 APLSLLLLCVDSORAEFTTVQSPASLSVATGEKVTIRCTSIDDDMMNMYQOKPGEP 64
OY 65 RLIIYDTSNRATGIPARFSGSGCTDPTLSTLSLEPEDFAVYCCQRFNFWPTFGGCTKV 124
DB 65 KLIISEGNTLRPGVPSRSSSGYGTDFEFTIENTLSEVDADYICLOSNDMPITFGAGTKL 124
OY 125 EFKRTVAAPSVFIIPPSEDEQLKSGTASVCLNNFPYPREAKVQKVDNALQSGNSQSVT 184
DB 125 ELKADAPTVSIFPPSSSEQLQANKATLVCLISDFPGAYTVAMKADSSPVYKAG--VET 184
OY 185 EQDSKSTYSLSSTLTLSKADYEKKHYACEVTHQGLSSPYTKSFNREGC 234
DB 185 DQDSKSTYSMSSTLTLTLDKDEYERHNSITCEATHTKSTSPYVKSFNRNEC 234
```

## RESULT 15

O8TBC9 PRELIMINARY: PRT: 233 AA.

```
AC O8TBC9. 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
```

DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)

```
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-B-cell;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC022823; AAH22823.1;
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00406; IGV_1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 233 AA; 24867 MW; 367411BFD6FADF92 CRC64;
```

Query Match 37.5%; Score 458.5; DB 4; Length 233;

Best Local Similarity 43.1%; Pred. No. 1.1e-35;  
Matches 100; Conservative 41; Mismatches 82; Indels 9; Gaps 6;

```
OY 7 LLLFLLLMLPDTGELVLTQSPATLSLSPGERATLACRASOTASRYLAWYQOQPGQAPRL 66
DB 6 LLLPLLTCTGSEASVYELTQ--PPSVSPGQTARITGSGDALPQYAYWYQKPGQAPVL 64
OY 67 LIYDTSNRATGIPARFSGSGCTDPTLSTLSLEPEDFAVYCCQ--QRFNFWPTFGGCTKV 124
DB 65 VIYKDNEPSSGIPERFSSSSGTYVTTLTISGVQAEDEADYICQASDSSGTYWVFGGTKL 124
OY 125 E-FKRTVAAPSVFIIPPSEDEQLKSGTASVCLNNFPYPREAKVQKVDNALQSGNSQSV 182
DB 125 TVLQGPRAAPSVYTLFPPSSSEELQANKATLVCLISDFPGAYTVAMKADSSPVYKAG--VET 182
OY 183 VTQDSKSTYSLSSTLTLSKADYEKKHYACEVTHQGLSSPYTKSFNREGC 234
DB 183 TTPSKQSNKKYAAASSYLSLTPEQWKSHKSYSCQVTHG--STVEKTVAPTEC 232
```

Search completed: September 12, 2003, 13:03:29  
Job time : 42.6525 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 12, 2003, 12:47:03 : Search time 9.91525 Seconds  
(without alignments)  
1109.830 Million cell updates/sec

Title: US-09-848-832-4  
Perfect score: 1223  
Sequence: 1 MEAPAQLLFLLLMLPDTTG.....EYTHGGLSSPYTKSFNRGRC 234

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	568	46.4	115	KV3J_HUMAN	P04437 homo sapien
2	563.5	46.1	129	KV3H_HUMAN	P04207 homo sapien
3	562.5	46.0	129	KV3M_HUMAN	P18136 homo sapien
4	553.5	45.3	129	KV3L_HUMAN	P18135 homo sapien
5	548	44.8	106	KAC_HUMAN	P01834 homo sapien
6	529	43.3	128	KV3K_HUMAN	P06311 homo sapien
7	494.5	40.4	116	KV3J_HUMAN	P04314 homo sapien
8	448.5	36.7	109	KV3B_HUMAN	P01620 homo sapien
9	448.5	36.7	109	KV3D_HUMAN	P01622 homo sapien
10	442.5	36.2	109	KV3E_HUMAN	P01623 homo sapien
11	441.5	36.1	109	KV3G_HUMAN	P04206 homo sapien
12	441.5	36.1	109	KV3G_HUMAN	P04206 homo sapien
13	432	35.3	134	KV4C_HUMAN	P06119 homo sapien
14	427.5	35.0	108	KV3A_HUMAN	P06119 homo sapien
15	427.5	35.0	133	KV3E_HUMAN	P06119 homo sapien
16	418	34.2	129	KV3I_HUMAN	P04432 homo sapien
17	417	34.1	129	KV3I_HUMAN	P04431 homo sapien
18	414	33.9	131	KV3I_MOUSE	P01661 mus musculu
19	409	33.4	132	KV3E_MOUSE	P01658 mus musculu
20	406	33.2	117	KV3L_HUMAN	P01602 homo sapien
21	400	32.7	108	KV3M_HUMAN	P01605 homo sapien
22	399.5	32.7	100	KV3C_HUMAN	P01621 homo sapien
23	393	32.1	108	KV3C_HUMAN	P01621 homo sapien
24	391.5	32.0	133	KV4B_HUMAN	P06130 homo sapien
25	387	31.6	108	KV3B_HUMAN	P06133 homo sapien
26	386	31.6	108	KV3B_HUMAN	P06133 homo sapien
27	384	31.4	108	KV3B_HUMAN	P04304 homo sapien
28	381	31.2	114	KV4A_HUMAN	P01603 homo sapien
29	379	31.0	108	KV3C_HUMAN	P01625 homo sapien
30	378	30.9	108	KV3C_HUMAN	P01595 homo sapien
31	377	30.8	128	KV3E_MOUSE	P01608 homo sapien
32	377	30.8	149	KV5A_MOUSE	P01633 mus musculu
33	376.5	30.8	107	KV3D_HUMAN	P01596 homo sapien

34	376	30.7	108	1	KV3I_HUMAN	P01606 homo sapien
35	376	30.7	136	1	KV5B_MOUSE	P01634 mus musculu
36	375	30.7	108	1	KV3E_HUMAN	P01597 homo sapien
37	374	30.6	108	1	KV3L_HUMAN	P01604 homo sapien
38	374	30.6	108	1	KV3L_HUMAN	P01610 homo sapien
39	372	30.4	111	1	KV3O_MOUSE	P01667 mus musculu
40	369	30.2	108	1	KV3O_HUMAN	P01607 homo sapien
41	367	30.0	106	1	KACB_RAT	P01835 rattus norv
42	367	30.0	108	1	KV3G_HUMAN	P01599 homo sapien
43	365	29.8	108	1	KV3S_HUMAN	P01611 homo sapien
44	364	29.8	108	1	KV3A_HUMAN	P01593 homo sapien
45	364	29.8	108	1	KV3Y_HUMAN	P80362 homo sapien

## ALIGNMENTS

```

RESULT 1
KV3I_HUMAN
ID KV3I_HUMAN STANDARD; PRT; 115 AA.
AC P04433;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region VG precursor (Fragmen!).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85087932; PubMed=6440122;
RA Pech M., Zachau H.G.;
RT "Immunoglobulin genes of different subgroups are ..interdigitated
   within the VK locus."
RL Nucleic Acids Res. 12:9229-9236(1984).
-----
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CC EMBL; X01668; -; NOT_ANNOTATED_CDS.
DR PIR; A01900; K3HUG.
DR HSSP; P80362; IWT.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding activity; NAS.
DR GO; GO:0006935; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 >115
FT DOMAIN 21 43 IG KAPPA CHAIN V-II REGION VG.
FT DOMAIN 44 54 FRAMEWORK-1.
FT DOMAIN 55 69 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 70 76 FRAMEWORK-2.
FT DOMAIN 77 108 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 109 115 FRAMEWORK-3.
FT DISULFID 43 108 COMPLEMENTARITY-DETERMINING-3.
FT NON_TER 115 115 BY SIMILARITY.
SQ
SEQUENCE 115 AA; 12575 MW; 2DE47CDA3A17D555 CRC64;

Query Match 46.4%; Score 568; DB 1; Length 115;
Best Local Similarity 93.9%; Pred. No. 3.1e-41;
Matches 108; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

```

QY 1 MEAPQAQLFLLLMLPDTTGEIVLTQSPATLSLSPGERATLACRASQTSRYLAWYQOKP 60  
Db 1 MEAPQAQLFLLLMLPDTTGEIVLTQSPATLSLSPGERATLACRASQTSRYLAWYQOKP 60  
QY 61 GOAPRLIYDTSNRATGIPARFSGSGGTFTLTISSLEPEDFAVYVYCOQRNMP 115  
Db 61 GOAPRLIYDASNRATGIPARFSGSGGTFTLTISSLEPEDFAVYVYCOQRNMP 115

## RESULT 2

KV3H\_HUMAN STANDARD; PRT; 129 AA.  
ID KV3H\_HUMAN  
AC P04207;  
DT 20-MAR-1987 (Rel. 04, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-II region CLL precursor (Rheumatoid factor).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=68177570; PubMed=3083417;  
RA Jirik F.R., Sarge J., Fong S., Heltmann J.G., Curo J.G., Chen P.P.,  
RA Goldfien R., Carson D.A.;  
RT "Cloning and sequence determination of a human rheumatoid factor  
RT light-chain gene."  
RL Proc. Natl. Acad. Sci. U.S.A. 83:2195-2199(1986).  
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DR EMBL; M12740; AAAS8992.1; -.  
DR HSSP; P80362; IWTL.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding activity; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro: IPR007110; Ig\_Like.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003596; Ig\_V.  
DR Pfam: PF00047; Ig; 1.  
DR SMART: SM00406; Igv; 1.  
DR PROSITE; PS50835; IG\_Like; 1.  
KW Immunoglobulin V region; Signal.  
FT SIGNAL 1 20  
FT CHAIN 21 129 IG KAPPA CHAIN V-II REGION CLL.  
FT DOMAIN 21 43 FRAMEWORK-1.  
FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 55 69 FRAMEWORK-2.  
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 77 108 FRAMEWORK-3.  
FT DOMAIN 109 118 COMPLEMENTARITY-DETERMINING-3.  
FT DOMAIN 119 129 JK1 SEGMENT.  
FT DISULFID 43 108 BY SIMILARITY.  
FT NON\_TER 129 129  
SQ SEQUENCE 129 AA; 14275 MW; 5C13B411BE60CC14 CRC64;

Query Match 46.1%; Score 563.5; DB 1; Length 129;  
Best Local Similarity 83.7%; Pred. No. 8.5e-41;  
Matches 108; Conservative 8; Mismatches 12; Indels 1; Gaps 1;

QY 1 MEAPQAQLFLLLMLPDTTGEIVLTQSPATLSLSPGERATLACRASQTSRYLAWYQOKP 60  
Db 1 MEAPQAQLFLLLMLPDTTGEIVLTQSPATLSLSPGERATLACRASQTSRYLAWYQOKP 60  
QY 61 GOAPRLIYDTSNRATGIPARFSGSGGTFTLTISSLEPEDFAVYVYCOQRNMP 115

Db 61 GOAPRLIYDTSNRATGIPARFSGSGGTFTLTISSLEPEDFAVYVYCOQRNMP 115  
QY 120 OCTKVEFKR 128  
Db 121 OCTKVEIKR 129

## RESULT 3

KV3M\_HUMAN STANDARD; PRT; 129 AA.  
ID KV3M\_HUMAN  
AC P18136;  
DT 01-NOV-1990 (Rel. 16, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-III region HIC precursor.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=68177307; PubMed=3127527;  
RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;  
RT "Autoantibody-associated kappa light chain variable region gene  
RT expressed in chronic lymphocytic leukemia with little or no somatic  
RT mutation. Implications for etiology and immunotherapy."  
RL J. Exp. Med. 167:840-852(1988).  
CC -1- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M  
CC AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC  
CC LEUKEMIA.  
DR PIR; P10021; K3HCHI.  
DR HSSP; P80362; IWTL.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding activity; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro: IPR007110; Ig\_Like.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003596; Ig\_V.  
DR Pfam: PF00047; Ig; 1.  
DR SMART: SM00406; Igv; 1.  
DR PROSITE; PS50835; IG\_Like; 1.  
KW Immunoglobulin V region; Signal.  
FT SIGNAL 1 20  
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION HIC.  
FT DOMAIN 21 43 FRAMEWORK-1.  
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 56 70 FRAMEWORK-2.  
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 78 109 FRAMEWORK-3.  
FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING-3.  
FT DOMAIN 119 129 JK1 SEGMENT.  
FT DISULFID 43 109 BY SIMILARITY.  
FT NON\_TER 129 129  
SQ SEQUENCE 129 AA; 14070 MW; 7395528EA2BB74D6 CRC64;

Query Match 46.0%; Score 562.5; DB 1; Length 129;  
Best Local Similarity 85.3%; Pred. No. 1e-40;  
Matches 110; Conservative 6; Mismatches 12; Indels 1; Gaps 1;

QY 1 MEAPQAQLFLLLMLPDTTGEIVLTQSPATLSLSPGERATLACRASQTSRYLAWYQOKP 59  
Db 1 MEAPQAQLFLLLMLPDTTGEIVLTQSPATLSLSPGERATLACRASQTSRYLAWYQOKP 60  
QY 60 PGQAPRLIYDTSNRATGIPARFSGSGGTFTLTISSLEPEDFAVYVYCOQRNMP 119  
Db 61 PGQAPRLIYDTSNRATGIPARFSGSGGTFTLTISSLEPEDFAVYVYCOQRNMP 120  
QY 120 OCTKVEFKR 128  
Db 121 OCTKVEIKR 129

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RESULT 4
KV3L_HUMAN          STANDARD:      PRT;      129 AA.
AC P18135;
DT 01-NOV-1990 (rel. 16, Created)
DT 01-NOV-1990 (rel. 16, Last sequence update)
DT 15-JUL-1999 (rel. 38, Last annotation update)
DE Ig kappa chain V-II region HAH precursor.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88171307; PubMed=3127527;
RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT "Autoantibody associated kappa light chain variable region gene
RT expressed in chronic lymphocytic leukemia with little or no somatic
RT mutation. Implications for etiology and immunotherapy.";
RL J. Exp. Med. 167:840-852(1988).
CC -1- DISASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
CC AUTANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCTIC
CC LEUKEMIA.
DR PIR: P10022; K3HUA.
DR HSSP: P80362; 1WTL.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding activity; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; I9-1like.
DR InterPro: IPR003006; I9_MHC.
DR Pfam: PF00047; I9_1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG-LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 129
FT CHAIN 21 129 IG KAPPA CHAIN V-II REGION HAH.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 56 70 FRAMEWORK-2.
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 78 109 FRAMEWORK-3.
FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 119 129 JKL SEGMENT.
FT DISULFID 43 109 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14073 MW; D3C5529272774D0 CRC64;

Query Match 45.3%; Score 553.5; DB 1; Length 129;
Best Local Similarity 85.3%; Pred. No. 5.9e-40;
Matches 110; Conservative 5; Mismatches 13; Indels 1; Gaps 1;

QY 1 MEPAQLLELLMLPDTTGEIVLQSPATLSISPERATLACRASQT-ASRYLAWYQOK 59
DB 1 METPAQLLELLMLPDTTGEIVLQSPATLSISPERATLACRASQSYSSSYLAWYQOK 60
QY 60 PQGARRLLYDTSNATGIPARFSGSGSTDTLTLSISLEPEDFANYTCQQRNFWPTG 119
DB 61 PQGARRLLYDTSNATGIPARFSGSGSTDTLTLSISLEPEDFANYTCQQRNFWPTG 120
QY 120 OCTKVEFKR 128
DB 121 OCTKVEIKR 129

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GN IGKC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE (MELOMA PROTEIN EU).
RX MEDLINE=71064023; PubMed=5469770;
RA Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. VI. Amino
RT acid sequence of the light chain.";
RL Biochemistry 9:3155-3161(1970).
RN [2]
RP DISULFIDE BONDS.
RX MEDLINE=71064027; PubMed=4923144;
RA Gall W.E., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. X.
RT Intrachain disulfide bonds.";
RL Biochemistry 9:3188-3196(1970).
RN [3]
RP SEQUENCE (BENCE-JONES PROTEIN TI).
RX MEDLINE=72188439; PubMed=5027703;
RA Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein
RT ti). IV. The complete amino acid sequence and its significance for
RT the mechanism of antibody production.";
RL Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=81042304; PubMed=6775818;
RA Hieter P.A., Max E.E., Seidman J.G., Maizel J.V. Jr., Leder P.;
RT "Cloned human and mouse kappa immunoglobulin constant and J region
RT genes conserve homology in functional segments.";
RL Cell 22:197-207(1980).
RN [5]
RP SEQUENCE (BENCE-JONES PROTEIN ROY).
RA Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H.,
RA Steimetz-Kayne M., Suter L., Watanabe S.;
RL (in) Franek F., Shugar D. (eds.);
RL Gamma globulins: structure and function, pp.57-74, Academic Press,
RL New York (1969).
RN [6]
RP SEQUENCE (BENCE-JONES PROTEIN CUM).
RX MEDLINE=68242259; PubMed=556923;
RA Hilschmann N.;
RT "The complete amino acid sequence of Bence Jones protein Cum (kappa-
RT type).";
RL Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).
RN [7]
RP SEQUENCE (BENCE-JONES PROTEIN AG).
RX MEDLINE=69234734; PubMed=4893682;
RA Titali K., Shinoda T., Putnam F.W.;
RT "The amino acid sequence of a kappa type Bence-Jones protein. 3. The
RT complete sequence and the location of the disulfide bridges.";
RL J. Biol. Chem. 244:3550-3560(1969).
RN [8]
RP SEQUENCE (WALDENSTROM'S MACROGLOBULIN OU).
RX MEDLINE=70201507; PubMed=5447531;
RA Kohler H., Shimizu A., Paul C., Putnam F.W.;
RT "Macroglobulin structure: variable sequence of light and heavy
RT chains.";
RL Science 169:56-59(1970).
RN [9]
RP SEQUENCE OF 1-33; 38-41 AND 62-80.
RP TISSUE-Abdominal adipose tissue;
RX PubMed=9588180;
RA Olsen K.E., Sletten K., Westermarck P.;
RT "Extended analysis of AL-amyloid protein from abdominal wall
RT subcutaneous fat biopsy: kappa IV immunoglobulin light chain.";
RL Biochem. Biophys. Res. Commun. 245:713-716(1998).
CC -1- MISCELLANEOUS: THE EU SEQUENCE HAS THE INV (3) ALLOTYPIC MARKER,
CC 45-ALA 6 83-VVL. THE ROY SEQUENCE HAS THE IIV (1,2) ALLOTYPIC

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CC CC      MARKER, 45-ALA AND 83-LEU.
CC - - - - - SIMILARITY: Contains 1 Immunoglobulin-like domain.
CC -----
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CC -----
DR EMBL: J00241; AAA58989.1; -.
DR EMBL: U00557; CA23823.1; -.
DR PIR: B90562; K3H0.
DR PDB: 1D5B; 09-FEB-00.
DR PDB: 1D5I; 09-FEB-00.
DR PDB: 1D6V; 04-OCT-00.
DR PDB: 1HEZ; 10-AUG-01.
DR PDB: 1HKL; 12-MAR-97.
DR PDB: 1I7Z; 08-AUG-01.
DR PDB: 1M1M; 15-MAY-97.
DR GeneW: HGNC:5716; IGKC.
DR MIM: 147200; -.
DR GO: GO:0003823; F:antigen binding activity; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-Like.
DR InterPro: IPR003597; Ig-CL.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00407; IGL; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
DR PROSITE: PS00290; IG_MHC; 1.
DR Immunoglobulin domain; Immunoglobulin C region; 3D-structure.
FT NON_TER 1 102 IG-LIKE.
FT DOMAIN 5 86
FT DISULFID 25 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT VARIANT 83 83 V->L (IN INV(1,2) MARKER).
FT VARIANT 83 83 /FTID-VAR.003897.
FT CONFLICT 14 14 D->N (IN REF. 7 AND 8).
FT CONFLICT 57 57 E->Q (IN REF. 5 AND 6).
SQ SEQUENCE 106 AA; 11609 MW; 51984D1FDD372CE8 CRC64;

Query Match 44.8%; Score 548; DB 1; Length 106;
Best Local Similarity 100.0%; Pred. No. 1.4e-39;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 129 TVAAPSVFIFPPSDEQLKSGTASVVCCLINFFPREAKYQMKVDNALGSGNSQESVTEGDS 188
DB 1 TVAAPSVFIFPPSDEQLKSGTASVVCCLINFFPREAKYQMKVDNALGSGNSQESVTEGDS 60

QY 189 KDSITYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 234
DB 61 KDSITYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 106

RESULT 6
KV3J_HUMAN STANDARD: PRT: 128 AA.
ID KV3J_HUMAN
AC P06311;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region IARC/BLA1 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041852; PubMed=2997711;
RA Klobbeck H.G., Meindl A., Combitato G., Solomon A., Zachau H.G.;
RT "Human Immunoglobulin kappa light chain genes of subgroups II and

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RT ILL.";
RL Nucleic Acids Res. 13:6499-6513(1985).
CC -----
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CC -----
DR EMBL: 200021; CA27316.1; -.
DR PIR: A01899; K3H041.
DR HSP: P01607; 1REI.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding activity; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-Like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
DR Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 128 IG KAPPA CHAIN V-III REGION IARC/BLA1.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 69 FRAMEWORK-2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 77 108 FRAMEWORK-3.
FT DOMAIN 109 117 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 118 128 JH1 SEGMENT.
FT DISULFID 43 128 BY SIMILARITY.
FT NON_TER 128 128
SQ SEQUENCE 128 AA; 14070 MW; C08957F0EB3B9012 CRC64;

Query Match 43.3%; Score 529; DB 1; Length 128;
Best Local Similarity 81.2%; Pred. No. 6.8e-38;
Matches 104; Conservative 6; Mismatches 18; Indels 0; Gaps 0;

QY 1 MEAPQQLFLFLILPDTGTGELVLTQSPATLSLSPGERATLACRASQTSRYLAWQKP 60
DB 1 METPAQLFLFLILPDTGTGELVLTQSPATLSLSPGERATLACRASQTSRYLAWQKP 60

QY 61 GQAPRLIYDPSNRATGIPARPSGSGDTFLTSLSLEPEDFAVYCOQRRNPWTGQ 120
DB 61 GQSPRLIRDASSRANGIPDRPSGSGDTFLTSLSLEPEDFAVYCOQRTSTPTGQ 120

QY 121 GTRVEFKR 128
DB 121 GTRKEIKR 128

RESULT 7
KV3J_HUMAN STANDARD: PRT: 116 AA.
ID KV3J_HUMAN
AC P04434;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region VH precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85087932; PubMed=6440122;
RA Pech M., Zachau H.G.;
RT "Immunoglobulin genes of different subgroups are interdigitated
RT within the VK locus.";
RL Nucleic Acids Res. 12:9229-9236(1984).

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CC or send an email to license@1sb-sib.ch).
CC -----
DR EMBL: X02725; -; NOT_ANNOTATED_CDS.
DR PIR: A01901; K3H0VH.
DR HSSP: P80362; 1WTL.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding activity; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
DR Immunoglobulin V region; Signal.
KW SIGNAL
FT CHAIN 1 20
FT DOMAIN 21 >116 IG KAPPA CHAIN V-II REGION VH.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 56 70 FRAMEWORK-2.
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 78 109 FRAMEWORK-3.
FT DOMAIN 110 116 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 43 109 BY SIMILARITY.
FT NON_TER 116 116
SQ SEQUENCE 116 AA; 12757 MW; 51CDS5BA53B21929 CRC64;

Query Match
Best Local Similarity 83.6%; Score 494.5; DB 1; Length 116;
Matches 97; Conservative 6; Mismatches 12; Indels 1; Gaps 1;

QY 1 MEAPADLLFLLLIMPDITGEIVLTSPATLSPEGRATLACRASQT-ASRYLAWYQOK 59
    |||||
DB 1 MEAPADLLFLLLIMPDITGEIVLTSPATLSPEGRATLACRASQVSSTYLYWYQOK 60
    |||||
QY 60 PGQAPRLIYDTSNPGATIPARFSGSGGTFDFTLSLEPEDFAVYCCQQRNMP 115
    |||||
DB 61 PGQAPRLIYDTSNPGATIPARFSGSGGTFDFTLSLEPEDFAVYCCQQRNMP 116
    |||||

RESULT 8
KV3D_HUMAN STANDARD; PRT; 109 AA.
ID P01620;
AC 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region SITE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=82046598; PubMed=6794615;
RA Andrews D.W., Capra J.D.
RT Amino acid sequence of the variable regions of light chains from two
RT idiotypically cross-reactive human Igm anti-gamma-globulins of the Wa
RT group.
RL Biochemistry 20:5816-5822(1981).
RC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC GLOBULIN ACTIVITY.
DR PIR: A01892; K3H0ST.
DR HSSP: P80362; 1WTL.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding activity; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR GO: GO:0003823; F:antigen binding activity; NAS.

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DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DISULFID 23 89 BY SIMILARITY.
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11775 MW; 7689C3E6CD46FB4 CRC64;

Query Match
Best Local Similarity 81.7%; Score 448.5; DB 1; Length 109;
Matches 89; Conservative 7; Mismatches 12; Indels 1; Gaps 1;

QY 21 EIVLTQSPATLSPEGRATLACRASQTASR-YLAWYQOK-PGQAPRLIYDTSNPGATIP 79
    |||||
DB 1 EIVLTQSPATLSPEGRATLACRASQVSNSYLAWYQOK-PGQAPRLIYDTSNPGATIP 60
    |||||
QY 80 ARFSGSGSGTDFLTLSISLEPEDFAVYCCQQRNMPWTFGJGTKEFKR 128
    |||||
DB 61 DRFSGSGSGTDFLTLSISLEPEDFAVYCCQQRNMPWTFGJGTKEFKR 109
    |||||

RESULT 9
KV3D_HUMAN STANDARD; PRT; 109 AA.
ID P01622;
AC 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region TI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=72188439; PubMed=5027703;
RA Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein
RT TI). IV. The complete amino acid sequence and its significance for
RT the mechanism of antibody production."
RL Hoppe-Sejler's Z. Physiol. Chem. 353:189-208(1972).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR: A01895; K3HUT1.
DR HSSP: P80362; 1WTL.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding activity; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DISULFID 23 89 BY SIMILARITY.
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11788 MW; 8C350586DC7749BC CRC64;

Query Match
Best Local Similarity 82.6%; Score 448.5; DB 1; Length 109;
Matches 90; Conservative 6; Mismatches 12; Indels 1; Gaps 1;

QY 21 EIVLTQSPATLSPEGRATLACRASQTASR-YLAWYQOK-PGQAPRLIYDTSNPGATIP 79
    |||||
DB 1 EIVLTQSPATLSPEGRATLACRASQVSNSYLAWYQOK-PGQAPRLIYDTSNPGATIP 60
    |||||
QY 80 ARFSGSGSGTDFLTLSISLEPEDFAVYCCQQRNMPWTFGJGTKEFKR 128
    |||||

```

```

RL Biochemistry 20:5816-5822(1981).
CC -I- MISCELLANEOUS; THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC GLOBULIN ACTIVITY.
DR PIR: A01896; K3HOWL.
DR HSSP: P80362; 1MTL.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding activity; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPRO07110; Ig-like.
DR InterPro: IPRO03006; Ig_MHC.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS00835; IG_LIKE; 1.
DR Immunoglobulin V region.
FT DISULEFID 23 89 BY SIMILARITY.
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11746 MW; 566C115E6B9CBBEE CRC64;

Query Match 36.1%; Score 441.5; DB 1; Length 109;
Best Local Similarity 81.7%; Pred. No. 1.3e-30;
Matches 89; Conservative 6; Mismatches 13; Indels 1; Gaps 1

QY 21 EIVLQSPATLSLSGERATACRASOR-ASRYLAWQKPGQAPRLLIYDTSNRATGIP 79
Db 1 EIVLRDSPEPTLSLSGERATISCRASVSQSGYLGMWQQAPGQAPRLLIGASSRRATGIP 60
80 AREFGSGSGTDFTLTSSILEPEDFAVYYYYCOQRFNMPWTFGQGKVEKKR 128
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:||
61 DRMSGSGSTDFTLTISRLEPEDFAVYYCYQQYGSLGRTPFGQKVEIKR 109

RESULT 12
KV3G_HUMAN STANDARD; PRT; 109 AA.
AC P04206;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
OS Ig kappa chain V-IIJ region GOL (Rheumatoid factor).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mamalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=86230578; PubMed=3086710;
RA Newkirk M., Chen P.P., Carson D.A., Posnett D., Capra J.D.;
RT "Amino acid sequence of a light chain variable region of a human
RT rheumatoid factor of the Wa idiotype group, in part predicted by its
RT reactivity with antipeptide antibodies."
RL Mol. Immunol. 23:239-244(1986).
PIR: A01893; K3HUGO.
DR HSSP: P80362; 1MTL.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding activity; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPRO07110; Ig-like.
DR InterPro: IPRO03006; Ig_MHC.
DR Pfam: PF00047; Ig_v.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS00835; IG_LIKE; 1.
DR Immunoglobulin V region.
FT DISULEFID 23 89 BY SIMILARITY.
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11830 MW; 9349A5BD93588B6 CRC64;

Query Match 36.1%; Score 441.5; DB 1; Length 109;
Best Local Similarity 80.7%; Pred. No. 1.3e-30;
Matches 88; Conservative 8; Mismatches 12; Indels 1; Gaps 1

21 EIVLQSPATLSLSGERATACRASOTASH-VYAWQKPGQAPRLLIYDTSNRATGIP 79

```

DB 1 MWLQTVFISLLNISGAYGDI VMTQSPDSLAVSLGERATINCKSSQSI LYSSDNKNYLA 60

RT III. "

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CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@sib-sib.ch).
CC      -----
DR      EMBL; 200020; CAA77315.1; .
DR      PIR; A01890; K2HURP.
DR      HSSP; P80362; 1M7L.
DR      GO; GO:0005576; C:extracellular; NAS.
DR      GO; GO:0003823; F:antigen binding activity; NAS.
DR      GO; GO:0006955; P:immune response; NAS.
DR      InterPro; IPR007110; IG-1like.
DR      InterPro; IPR003006; IG_MHC.
DR      InterPro; IPR003596; IG_V.
DR      Pfam; PF00047; Ig; 1.
DR      SMART; SM00406; IGV; 1.
DR      PROSITE; PS50835; IG_LIKE; 1.
KW      Immunoglobulin V region; Signal.
FT      SIGNAL 1 20
FT      CHAIN 1 133
FT      DOMAIN 21 133 IG KAPPA CHAIN V-II REGION RPM1 6410.
FT      DOMAIN 21 43 FRAMEWORK-1.
FT      DOMAIN 44 59 COMPLEMENTARITY-DETERMINING-1.
FT      DOMAIN 60 74 FRAMEWORK-2.
FT      DOMAIN 75 81 COMPLEMENTARITY-DETERMINING-2.
FT      DOMAIN 82 113 FRAMEWORK-3.
FT      DOMAIN 114 122 COMPLEMENTARITY-DETERMINING-3.
FT      DOMAIN 123 132 FRAMEWORK-4.
FT      DISULFID 43 113 BY SIMILARITY.
FT      NON_TER 133 133
SQ      SEQUENCE 133 AA; 14707 MW; 513CAFA3673009EE CRC64;

Query Match 35.0%; Score 427.5; DB 1; Length 133;
Best Local Similarity 58.6%; Pred. No. 2.5e-29;
Matches 78; Conservative 24; Mismatches 26; Indels 5; Gaps 1;

OY      1 MEAPALFLFLLLMLPDTGEIVLTQSPATLSLSPGERATLACRASQT-----ASRYLAW 55
DB      1 MRLPAQLGLMLMWPGSSCDVMTQSPLSLPYTLGQPASISCRSSQSLVYSDGNTYLLNW 60
OY      56 YQAKFGQAPRLLIYDTSNRATGIPARFSGSGSGTDFTLSSLEPEDFAVYYCQGRFNP 115
DB      61 FQQRPGQSPRRILYKVSNRDSGVDPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQGTWMS 120
OY      116 WTFGGGTKEFKR 128
DB      121 WTFGGGTKEFKR 133
```

Search completed: September 12, 2003, 13:01:16  
Job time : 10.9153 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 12, 2003, 12:57:09 : Search time 17.5169 seconds  
(without alignments)  
1284.668 Million cell updates/sec

Title: US-09-848-832-4

Perfect score: 1223

Sequence: 1 MEAPAQQLFLILLMLPDTTG.....EVTHQGLSSPYTKSPFNRECC 234

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1010.5	82.6	215	2 JE0242	Ig kappa chain NIG
2	983.5	80.4	215	2 JE0244	Ig kappa chain NIG
3	971.5	79.4	215	2 JE0243	Ig kappa chain NIG
4	944.5	77.2	215	2 A23746	Ig kappa chain V-I
5	848	69.3	216	2 JE0241	Ig kappa chain Am3
6	771	63.0	240	2 S06084	Ig kappa chain pre
7	727	58.4	234	2 S01320	Ig kappa chain pre
8	717	58.6	234	2 S14237	Ig kappa chain pre
9	703.5	57.5	230	2 S3161	Ig kappa chain - s
10	702.5	57.4	219	2 S38865	Ig kappa chain - m
11	702.5	57.4	225	2 S37484	Ig kappa chain - m
12	702	57.4	218	2 S68241	Ig kappa chain V r
13	696	56.9	218	2 JCS810	Ig kappa chain V r
14	695	56.8	144	2 PLO106	Ig kappa chain pre
15	695	56.8	220	2 A31790	Ig kappa chain V r
16	692.5	55.6	235	2 S25058	Ig kappa chain - m
17	681.5	55.7	219	2 PC4203	Ig kappa chain (no
18	681.5	55.7	219	2 S52028	Ig kappa chain - m
19	678.5	55.5	225	2 JLO029	Ig kappa chain pre
20	677.5	55.4	217	2 S42722	Ig kappa chain - m
21	673.5	55.1	214	2 S16112	Ig kappa chain V r
22	672	54.9	219	2 S68212	Ig kappa chain (Ma
23	667	54.5	210	2 A56169	Ig kappa chain V r
24	613.5	50.2	135	2 S52059	Ig kappa chain V r
25	610	48.9	178	2 PTO219	Ig kappa chain V-C
26	609	48.8	128	2 S40379	Ig kappa chain V-J
27	600	48.1	128	2 A56701	Ig kappa chain V r
28	588.5	48.1	145	2 S20631	Ig kappa chain - h
29	584	47.8	125	2 S40344	Ig kappa chain V-J

30	582	47.6	129	2 S29627	Ig kappa chain V r
31	575.5	47.1	197	2 S29593	Ig kappa chain (W)
32	569	46.5	128	2 S40345	Ig kappa chain V-J
33	568	46.4	115	1 K3HVG	Ig kappa chain pre
34	565	46.2	128	2 S40343	Ig kappa chain V-J
35	563.5	46.1	229	2 A20969	Ig kappa chain pre
36	562.5	46.0	129	1 K3HUI	Ig kappa chain pre
37	562.5	46.0	129	2 S40363	Ig kappa chain - h
38	553.5	45.3	129	1 K3HHA	Ig kappa chain pre
39	552.5	45.2	129	1 S49532	anti-sm antibody V
40	548	44.8	106	1 K3HU	Ig kappa chain C r
41	547.5	44.8	128	2 S20636	Ig kappa chain V r
42	546.5	44.7	238	2 A49633	Ig lambda-like cha
43	545	44.6	111	2 S23628	Ig kappa chain V r
44	545	44.6	115	2 S11697	Ig kappa chain pre
45	544.5	44.5	131	2 S40328	Ig kappa chain - h

## ALIGNMENTS

## RESULT 1

JE0242

Ig kappa chain NIG26 precursor - human

C/Species: Homo sapiens (man)

C/Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 21-Jan-2000

C/Accession: JE0242

R:Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda

submitted to JIPID, November 1998

A/Description: Structure relationship of kappa type light chains with AL amyloidosis:

A/Reference number: JE0241

A/Accession: JE0242

A/Molecule type: protein

A/Residues: 1-215 <ALI>

C/Superfamily: Immunoglobulin V region; immunoglobulin homology

F:16-91/Domain: Immunoglobulin homology <IMV>

Query Match 82.6%; Score 1010.5; DB 2; Length 215;

Best Local Similarity 91.6%; Pred. No. 1.1e-62;

Matches 197; Conservative 4; Mismatches 13; Indels 1; Gaps 1;

OY	21	EVLTGSPATLSLSPERATLACRASQTS-RLYAWQKPGQAPRLIYDSNRATGIP	79
DB	1	EIVLTGSPATLSLSPERATLACRASQTSNNIYAWQKPGQAPRLIYDASRRATGIP	60
OY	80	ARFSGSGSTDFLTSLSSLEPEDFAVYQCQRENMWPTFGJGTRVEFKRTVAAPSVFIRP	139
DB	61	DRFSGSGSTDFLTSLSSLEPEDFAVYCCQYDRPWPFGJGTRVEIKRTVAAPSVFIRP	120
OY	140	PSDEOLKSGTASVCLNNFYPREAKVQKVDNALOSGNSDESVTEDSKDSTYSLSSTL	199
DB	121	PSDEOLKSGTASVCLNNFYPREAKVQKVDNALOSGNSDESVTEDSKDSTYSLSSTL	180
OY	200	TLSKADYEKKHYACEVTHQGLSSPYTKSPFNRECC	234
DB	181	TLSKADYEKKHYACEVTHQGLSSPYTKSPFNRECC	215

## RESULT 2

JE0244

Ig kappa chain NIG2 precursor - human

C/Species: Homo sapiens (man)

C/Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 21-Jan-2000

C/Accession: JE0244

R:Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yanagata, F.; Yamaki, S.; Kazi, H.

submitted to JIPID, November 1998

A/Description: A new subgroup of k type light chains (VK) identified in cases of AL

A/Reference number: JE0243

A/Accession: JE0244

A/Molecule type: protein

A/Residues: 1-215 <ALI>

C/Superfamily: Immunoglobulin V region; immunoglobulin homology

F:16-90/Domain: Immunoglobulin homology <IMV>

[illegible][illegible]

G:SuperfamilyImmunoglobulin V region: immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-91/Domain: Immunoglobulin homology <IIM>  
  
Query Match 77.2%; Score 944.5; DB 2; Length 215;  
Best Local Similarity 89.7%; Pred. No. 3.6e-56;  
Matches 192; Conservative 6; Mismatches 15; Indels 1; Gaps 1;  
  
QY 21 EIVLTQSPATLSISPGERATLACRASQT-ASRYLAWYQOKPGQAPRLITYDTSNRAGCIP 79  
Db 1 EIVLTQSPATLSISPGERATLSGCGASGVSSNYTLAWYQOKPGQAPRLITYDASSRAGCIP 60  
  
QY 80 ARFGSGSGGDTFTLSISLSLEPEDFAVYVYCOOQRFNMWPTFGQGTVEEKRTVAASVEIFP 139  
Db 61 DRFGSGSGGTFETLTISRLEPEDFAVYVYGOQYSSPFTFGGQTKVEIKRTVAASVEIFP 120  
  
QY 140 PSDQLKSGTASVYCLNNFYPREAKYQWKVDNALQSGNSQESTPDDSDSPYSLSSLT 199  
Db 121 PSDQLKSGTASVYGLNNFTPREAKYQWKVDNALQSGNSQESTPEDSKDSTYSLSSLT 180  
  
QY 200 TLSRADYEKHKVACEVTHQGLSSPYTSFNNGE 233  
Db 181 TLSRADYEKHKVYAGEVTHQGLSSPYTSFNNGE 214

```

RESULT 5
JE0241
lg kappa chain Am37 precursor - human
C|Species: Homo sapiens (man)
C|Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C|Accession: JE0241
R|Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takada, K.; Kojima, M.; Takashi, I.; Shinoda
submitted to JIPIID, November 1998
A|Description: Structure relationship of kappa type light chains with AL amyloidosis:
A|Reference number: JE0241
A|Accession: JE0241
A|Molecule type: protein
A|Residues: 1-216 <ALIT>
C|Superfamily: Immunoglobulin V region: immunoglobulin homology .
F:Ig-92/Domain: Immunoglobulin homology <IMM>

Query Match          69.3%; Score 848; Db 2; Length 216;
Best Local Similarity 76.6%; Pred. No. 1,6e+51;
Matches 167; Conservative 23; Mismatches 22; Indels    6; Gaps   3;

Oy      21 EIVLTOSPATLSLSPGERATIACRASQT---ASRYLAHYQKPGAPRLLIYDTSNRA?T 76
       :||||||:::|| |||||: |::::: |: ||||| |||||: |||: | | : 
Db      1 DIVLTOSDPFLAVSLGERRATINCKSSQSVALYNKNPFIAMVQOKPGQC-PKLIIW-ANRES 58
               |||||MLQAEILVAAYTCQQYSTPYSFSGGGHLEIKRTVAAPSVF

Oy      77 GIAPRFSGSNGCPFTLTISLSLEPEDPAVVYYCCOOERFMMPMTFGCGTVVEKKRYAAPSVF 136
       ::||| ||||| |||||: ||| |||||:: |||||:: |||||:: ||||| |||||
Db      59 GVPRFRFSQGVDPTFLTISMQLAEILVAAYTCQQYSTPYSFSGGGHLEIKRTVAAPSVF 118
               ||||| ||||| |||||: ||| |||||:: |||||:: ||||| |||||

Oy     137 IFPPSDQLKSGTASVYCLLNPFYPREAKVQWKMDNALOGNSNQESYTEODSKDSITYSL 196
       |||||IFPPSDQLKGSTASVYCLLNPFYPREAKVQWKMDNALOGNSNQESTEDSKDSITYSL 178
Db     119 IFPPSDQLKSGTASVYCLLNPFYPREAKVQWKMDNALOGNSNQESYTEODSKDSITYSL 178
               |||||IFPPSDQLKGSTASVYCLLNPFYPREAKVQWKMDNALOGNSNQESTEDSKDSITYSL 178

Oy     197 STLTLRKADYEKHKVYAACEVTTHOGLSSPVTKSENRGCC 234
       || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     179 STLTLRSKADYEKHKVYAACEVTTHOGLSSPVTKSENRGCC 216
               || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 6
S06084
Ig kappa chain precursor - rat
C|Species: Rattus norvegicus (Norway rat)
C|Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jan-2000
C|Accession: S06084
R|Crowe, J.S.; Smith, M.A.; Cooper, H.J.
Nucleic Acids Res. 17, 7992, 1989
A>Title: Nucleotide sequence of Y3-Ag 1.2.3. rat myeloma immunoglobulin kappa chain c
A|Reference number: S06084; MIDB:90016888; PMID:2508067

```



Qy	185	EQDSKDYSLSTLTLSKRDYEKKHKVYACEVTHQGLSSPVTSFNRGEC	234
	:		
Db	181	DQDSKSTYSLSTLTLSSEYQSHNAVACEVSHKSLPTALVSNFNKNEC	230

## RESULT 10

Ig kappa chain - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 15-Jun-2001  
 C:Accession: S38865  
 R:R1KP, B.: Becker, W.; Schlaak, M.  
 Submitted to the EMBL data library, November 1993  
 A:Description: Combination of a defined specificity and desired isotype by cloning of an  
 A:Reference number: S38864  
 A:Accession: S38865  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-219 <R1P>  
 A:Cross-References: EMBL:Z27396; NID:g416538; PIDN:CAAB1787.1; PID:g416539  
 A:Superfamily: Immunoglobulin Y region; Immunoglobulin homology  
 :Keywords: heterotetramer; Immunoglobulin

Query Match	57.4%;	Score 702.5;	DB 2;	Length 219;
Best Local Similarity	59.8%;	Pred. No. 1.6e-41;		
Matches 131;	Conservative 35;	Mismatches 48;	Indels 5;	Gaps 11;

[illegible]

## RESULT 11

S37484 Ig kappa chain - mouse (fragment)  
S37484 C:Species: Mus musculus (house mouse)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 11-Jan-2000  
C:Accession: S37484  
R:Ducancel, F.F.D.  
submitted to the EMBL Data Library, February 1993  
A:Reference number: S37483  
A:Accession: S37484  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-225 <DUC>  
A:Cross-references: EMBL:X70424; NID:g406254; PIDD:CAA9866.1; PID:g406255  
C:Superfamily: Immunoglobulin V region; Immunoglobulin  
C:Keywords: heterotetramer; immunoglobulin  
homology

Query Match	57.4%;	Score 702.5;	DB 2;	Length 225;
Best Local Similarity	58.9%;	Pred. No. 1.6e-41;		
Matches 132;	Conservative 37;	Mismatches 54;	Indels 1;	Gaps 1;

[illegible]

QY 131 AAPSVEFPSPDEQLKSGTASVVCLLNFPYPREAKVQWKVDNALSGNSQESVTEQDSKD 190  
111:1 11111 111 11 1111 11111: 1:1:1 : : 1 1:11111  
Db 122 AAPTVSIFPPSSSEQLTSGGASVVCCLNFPKIDINWKWKIDGSEKRONGVLSWTDQSKD 181

## 12

RESULT 12  
S68241  
Ig kappa chain V region (Mab13-1) - mouse (fragment)  
N:Alternate names: Immunoglobulin light chain  
C:Species: Mus musculus (house mouse)  
C:Date: 24-Aug-1996 #sequence\_rev1010 13-Mar-1997 #text\_change 20-Jun-2000  
C:Accession: S68241; S68214  
R:Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, S.  
A:Submitted to the EMBL Data Library, March 1994  
A:Description: Specific peroxidase activity by formation of an antibody L-chain-porphyrin complex  
A:Reference number: S68241  
A:Accession: S68241

Residues: 1-218 <TAK>  
Cross-References: EMBL:D29670; NID:g473962; PIDD:BAA06141.1; PID:g473963  
TAKagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka,  
SBS Lett. 375, 273-276, 1995  
Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyrin  
Reference number: S68211; NUID:96085223; PMID:7498516

```
A>Status: nucleic acid sequence not shown
A:Accession: S06214
A:Molecule type: mRNA
A:Residues: 'N1','3-212 '<TAM>'
A:Cross-references: EMBL:D29670
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: Immunoglobulin

Query Match      57.4%; Score 702; DB 2; Length 218;
Best Local Similarity 61.0%; Pred. No. 1.7e+41;
Matches 133; Conservative 32; Mismatches 49; Indels 4; Gaps 1

QY    21 ELVTGSPATSLISPERGATTLACRASQSRA-----LYAYOQRKGQAPRLIYDTSNRAT 76
   |||||:::||:||||::::|:| | | :|||::| | | | | | | | | | | | | | | | | |
Db     1 ELVLTGSPASLAIVLSIGQRATITSCRSKRVSVASGYTIMHWYOQRKGQRPKLILSIAITLES 60

QY    77 GDPARTSGSGSGDTFTLSSLEPEDFAVVYYCOQRFNMWPMTFGGTVEERKTVAAPSVF 136
   |||||::||::|||::| | ::|||::| | | | | | | | | | | | | | | | | |
Db     61 GVPARSRSGSGSDPTFLNIHPVEEDVATYYCQHRSRELPPLTFAGGTAKTELKRDAAPTYS 120

QY    137 IPPPSDEQLKSGTASYVCLLNFFRYEAKKVOMKYDNALQSGNSOSEVTEBDSKDSTYSLS 196
   |||||::|| | ||| |||||::| | ::| | ::| | ::| | ::| | ::| | ::| | ::|
Db     121 IPPPSSEOLTSGASAVCFLLNFYPKDDINVMKKIDGSERONGVLNSWTDDSKDYTSMS 180

QY    197 STILTSLADYEKKHXYACEVTHQGILSSPVYTSPFNREGC 234
   |||||::| | ::| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     181 STLTKLDYEERHNSTYCEATHKSTSPVETSPFNNGCC 218
```

## RESULT 13

UC5810  
monoclonal antibody 13-1 light chain - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 04-Feb-1998 #sequence\_revision 13-Mar-1998 #text\_change 21-Jan-2000  
C/Accession: JC5810  
R/Akashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Harada, R.; Biochem. Biophys. Res. Commun. 240, 566-572, 1997  
A/Title: Structural characterization of mouse monoclonal antibody 13-1 against a porph  
A/Reference number: JC5810; MUID:98063277; PMID:9398605  
A/Accession: JC5810  
A/Molecule type: protein  
A/Residues: 1-218 <AKA>  
C/Comment: This catalytic antibody has peroxidase oxidase. It is directed against a p  
C/Superfamily: Immunoglobulin V region; Immunoglobulin homology <IM>  
C/16-94/Domain: Immunoglobulin homology <IM>



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OW protein - protein search, using sw model

Run on: September 12, 2003, 13:00:49 ; Search time 30.7966 Seconds  
(without alignments)  
2245.783 Million cell updates/sec

Title: US-09-848-832-3  
Perfect score: 2514  
Sequence: 1 MEFGSLWFLVAILKGVOCE.....MHEALHNHYTKSLSPGK 474

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 541936 seqs, 145912426 residues  
Total number of hits satisfying chosen parameters: 541936

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA:\*

1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*  
6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep:\*  
7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*  
8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*  
9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep:\*  
10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep:\*  
12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*  
13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*  
14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*  
15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*  
17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*  
18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2514	100.0	474	US-10-225-108A-3	Sequence 3, Appl1
2	2514	100.0	474	US-09-848-832-3	Sequence 3, Appl1
3	2279	90.7	449	US-09-736-371B-21	Sequence 21, Appl1
4	2257	89.8	451	US-09-832-698A-26	Sequence 26, Appl1
5	2249	89.5	444	US-10-150-475A-6	Sequence 6, Appl1
6	2196	87.4	470	US-10-020-786-9	Sequence 9, Appl1
7	2196	87.4	470	US-10-227-694-5	Sequence 5, Appl1
8	2193	87.3	452	US-09-726-258-71	Sequence 71, Appl1
9	2187	87.0	476	US-10-020-786-11	Sequence 11, Appl1
10	2183	86.8	478	US-09-948-429B-8	Sequence 8, Appl1
11	2183	86.8	478	US-10-124-807-8	Sequence 8, Appl1
12	2183	86.8	478	US-10-124-805-8	Sequence 8, Appl1
13	2181	86.8	449	US-10-356-974-2	Sequence 2, Appl1
14	2181	86.8	449	US-10-253-366-2	Sequence 2, Appl1
15	2181	86.8	449	US-10-316-694-2	Sequence 2, Appl1

16	2178	86.6	453	9	US-09-802-077-8	Sequence 8, Appl1
17	2178	86.6	453	9	US-09-802-096-8	Sequence 8, Appl1
18	2178	86.6	453	11	US-09-925-179-8	Sequence 18, Appl1
19	2173	86.4	451	9	US-09-920-171-18	Sequence 18, Appl1
20	2173	86.4	451	12	US-10-113-996-18	Sequence 18, Appl1
21	2173	86.4	451	12	US-10-292-869-2	Sequence 2, Appl1
22	2173	86.4	451	12	US-09-792-938-2	Sequence 3, Appl1
23	2171	86.4	463	15	US-10-153-382-3	Sequence 14, Appl1
24	2170	86.3	451	9	US-09-920-171-14	Sequence 16, Appl1
25	2170	86.3	451	9	US-09-920-171-16	Sequence 16, Appl1
26	2170	86.3	451	11	US-09-925-179-65	Sequence 65, Appl1
27	2170	86.3	451	12	US-10-113-996-14	Sequence 14, Appl1
28	2170	86.3	451	12	US-10-113-996-16	Sequence 16, Appl1
29	2170	86.3	464	15	US-10-153-382-9	Sequence 9, Appl1
30	2168	86.3	463	15	US-10-153-382-13	Sequence 13, Appl1
31	2167	86.2	451	11	US-09-925-179-66	Sequence 66, Appl1
32	2165	86.1	463	15	US-10-153-382-5	Sequence 5, Appl1
33	2161	86.0	451	11	US-09-925-179-68	Sequence 68, Appl1
34	2159	85.9	470	10	US-09-859-053-32	Sequence 32, Appl1
35	2157	85.8	470	10	US-09-859-053-36	Sequence 36, Appl1
36	2145	85.3	470	15	US-10-216-484-157	Sequence 157, Appl1
37	2134	84.9	470	15	US-10-216-484-147	Sequence 147, Appl1
38	2133	84.9	731	10	US-09-825-012-46	Sequence 46, Appl1
39	2133	84.9	741	10	US-09-825-012-55	Sequence 55, Appl1
40	2133	84.8	470	15	US-10-216-484-145	Sequence 145, Appl1
41	2131	84.8	470	15	US-10-216-484-143	Sequence 143, Appl1
42	2128	84.7	729	10	US-09-825-012-52	Sequence 52, Appl1
43	2128	84.7	739	10	US-09-825-012-51	Sequence 51, Appl1
44	2128	84.6	470	15	US-10-216-484-117	Sequence 117, Appl1
45	2125	84.5	467	15	US-10-171-452A-41	Sequence 41, Appl1

## ALIGNMENTS

RESULT 1									
US-10-225-108A-3									
Sequence 3, Application US/10225108A									
Publication No. US20030157112A1									
GENERAL INFORMATION:									
APPLICANT: HOOVER, Craig									
APPLICANT: DIETRICHOLD, Bernhard									
TITLE OF INVENTION: Recombinant Antibodies, and Compositions									
FILE REFERENCE: 8321-110									
CURRENT APPLICATION NUMBER: US/10/225,108A									
CURRENT FILING DATE: 2003-04-10									
PRIOR APPLICATION NUMBER: US 09/848,832									
PRIOR FILING DATE: 2001-05-04									
PRIOR APPLICATION NUMBER: US 60/204,518									
PRIOR FILING DATE: 2001-05-16									
PRIOR APPLICATION NUMBER: US 60/314,023									
PRIOR FILING DATE: 2001-08-21									
NUMBER OF SEQ ID NOS: 16									
SOFTWARE: FastSeq for Windows Version 4.0									
SEQ ID NO 3									
LENGTH: 474									
TYPE: PRT									
ORGANISM: Homo sapiens									
US-10-225-108A-3									
Query Match									
Best Local Similarity 100.0%; Score 2514; DB 12; Length 474;									
Matches 474; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
OY	1	MEFGSLWFLVAILKGVOCEVOLLDSGGGLVPGGSLRLSTAAAGFTFSNVMSWVROAP	60						
DB	1	MEFGSLWFLVAILKGVOCEVOLLDSGGGLVPGGSLRLSTAAAGFTFSNVMSWVROAP	60						
OY	61	KGLEWVAISASGSHSTYLAOSVKGRFTISRDNKNTLYLWNSLRADFTAVYCAKRE	120						
DB	61	KGLEWVAISASGSHSTYLAOSVKGRFTISRDNKNTLYLWNSLRADFTAVYCAKRE	120						

QY	121	WTMTVLVNGCFPYWMOGFRVTVYSASASTKCRPSVPLPRLAPSSKSTISGTAALGCLYKDYRPREP	180
Db	121	VTMTVLVNGGFPYWMOGFRVTVYSASASTKCRPSVPLPRLAPSSKSTISGTAALGCLYKDYRPREP	180
QY	181	VTWSNNSGALTSGVHTFPVALOSSGLYSLSSVTVAPSSLSGQTYICNNHRSNNKYDK	240
Db	181	VTWSNNSGALTSGVHTFPVALOSSGLYSLSSVTVAPSSLSGQTYICNNHRSNNKYDK	240
QY	241	RVEPRKCDKTHTCPRCPAPABELLGGPSVLEFPKPKDTLMSRPEVTCVAVDVSHEDEPY	300
Db	241	RVEPRKCDKTHTCPRCPAPABELLGGPSVLEFPKPKDTLMSRPEVTCVAVDVSHEDEPY	300
QY	301	KFNMYVDGVEVHNAAKTKPREQYNSTYRVVSVLTVLHODMLNGEKYCKVSNKALPAPTE	360
Db	301	KFNMYVDGVEVHNAAKTKPREQYNSTYRVVSVLTVLHODMLNGEKYCKVSNKALPAPTE	360
QY	361	KTISKAKQPRPQVYTLRPPSRNEEMTKNOVSLTCLYKGYRPSDIAEVESNGOPENNYYKT	420
Db	361	KTISKAKQPRPQVYTLRPPSRNEEMTKNOVSLTCLYKGYRPSDIAEVESNGOPENNYYKT	420
QY	421	TRPVLDGSGSFYLSKLTVDKSRMOOGANFSCSVNHEALHNHYTQKSLSLSPCK	474
Db	421	TRPVLDGSGSFYLSKLTVDKSRMOOGANFSCSVNHEALHNHYTQKSLSLSPCK	474

```

RESULT 2
US-09-848-832-3
: Sequence 3, Application US/09848832
: Publication No. US20030165507A1
: GENERAL INFORMATION:
: APPLICANT: Hoeper, Douglas
: APPLICANT: Dietzschold, Bernhard
: TITLE OF INVENTION: RABIES VIRUS-SPECIFIC NEUTRALIZING HUMAN
: FILE REFERENCE: H0001.NP0002
: CURRENT APPLICATION NUMBER: US/09/848, 832
: CURRENT FILING DATE: 2001-05-04
: PRIOR APPLICATION NUMBER: 60/204, 518
: PRIOR FILING DATE: 2000-05-16
: NUMBER OF SEQ ID NOS: 8
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 3
: LENGTH: 474
: TYPE: PRT
: ORGANISM: Homo sapien
US-09-848-832-3

Query Match          100.0%; Score 2514; DB 12; Length 474;
Best Local Similarity 100.0%; Pred. No. 3.4e-165;
Matches 474; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  MEFGLSWLFLVAIIKGVOCCEVOLLBSGGGLVOPGSLRUSCAASGFTFSNYAMSWVROAP 60
DB      1  MEFGLSWLFLVAIIKGVOCCEVOLLBSGGGLVOPGSLRLSCAASGFTFSNYAMSWVROAP 60
QY      61  GKGLEWVAISASGSHSTYLADSVKGFRTSRDNRKNTLYLQNMSLAEPTAVVYCAADRE 120
DB      61  GKGLEWVAISASGSHSTYLADSVKGFRTSRDNRKNTLYLQNMSLAEPTAVVYCAADRE 120
QY      121  VTMIIVLNGGFDYWGQGTATVVSASTKGPVSEPLAPSSKSTSGCTAALGLVKDYPREP 180
DB      121  VTMIIVLNGGFDYWGQGTATVVSASTKGPVSEPLAPSSKSTSGCTAALGLVKDYPREP 180
QY      181  VTVSMNAGALNSGHTTFAVYVLOSSGLYLSLSVYTVVSSSLGTQTYICNNHAKPSNTRYDK 240
DB      181  VTVSMNAGALNSGHTTFAVYVLOSSGLYLSLSVYTVVSSSLGTQTYICNNHAKPSNTRYDK 240
QY      241  RVEKRSCKDTHTCPCPAPELLGSPVFLFPPKPKDTLMSRPEVTCVVVDVSHEDPEV 300
DB      241  RVEKRSCKDTHTCPCPAPELLGSPVFLFPPKPKDTLMSRPEVTCVVVDVSHEDPEV 300
QY      301  KFNMYVDGVEVHNAKTRPEQYNSTRVSVLYLVLDQMLNGEKVKCVSNALPAPIE 360
DB      301  KFNMYVDGVEVHNAKTRPEQYNSTRVSVLYLVLDQMLNGEKVKCVSNALPAPIE 360

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Db	30	KFMWYDVGVENNAKTRPREDEYNSTRVAVSVLTVLHQMDLNGKREYKCKVCNKALPAPIE	366
Qy	361	KTISKAKGQREPOVYTLPRSPREEMTKNOVSLTCLYKRPESDIAVEKESGOENNYKT	420
Db	361	KTISKAKGQREPOVYTLPRSPREEMTKNOVSLTCLYKRPESDIAVEKESGOENNYKT	420
Qy	421	TPPYLDSGGSFLYSKLYVDSKRWQGNVFCSSVMHEALAHNYTQKSLUSPGK	474
Db	421	TPPYLDSGGSFLYSKLYVDSKRWQGNVFCSSVMHEALAHNYTQKSLUSPGK	474

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RESU/L 3
US-09-736-371B-21
; Sequence 21, Application US/09736371B
; Patent No. US20020131968A1
; GENERAL INFORMATION:
; APPLICANT: Waldmann, Herman
; APPLICANT: Frewin, Mark
; TITLE OF INVENTION: ACYCLOSYLATED ANTIBODIES
; FILE REFERENCE: Waldmann
; CURRENT APPLICATION NUMBER: US/09/736,371B
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: 9815909.8
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: PCT/GB99/02380
; PRIOR FILING DATE: 1999-07-21
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 21
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-736-371B-21

```

Query Match	90.7%	Score 2279;	DB 10;	Length 449;
Best Local Similarity	94.5%;	Pred. No. 4.7e-149;		
Matches 430; Conservative	8;	Mismatches 11;	Indels 6;	Gaps 1

Qy	20	EYOLLESGGGLVOPGGSLRLSCAAGPFNFNSAMSWAOAGKGLLWVMSALMSAGSHTYL	79
Dd	1	EYOLLESGGGLVOPGGSLRLSCAAGFTTFSSPPMAWNOAQAGKGLEWSTLSTSGGRTTY	60
Qy	80	ADSVKGRFTISRDNKNTLYLOMNSLRABDTAVYYCAKADREVMTIIVLNGGFDYWGQGR	139
Dd	61	RDSVKGRFTISRDNKNTLYLOMNSLRABDTAVYYCAAFRQ-----YSGGFDYWGQGT	114
Qy	140	VYVYSASTGPGVYFPLAPSSKSTSGGTALGLCYKDYFPEVYVYSNMSGALTSYHTFPA	199
Dd	115	VYVYSASTGPGVYFPLAPSSKSTSGGTALGLCYKDYFPEVYVYSNMSGALTSYHTFPA	174
Qy	200	VLOSGLYSLSSVYVYPPSSSLGTQYIICNVNHKFSNFKVDKRYEPKSCDPTHTCCPCPAP	259
Dd	175	VLOSGLYSLSSVYVYPPSSSLGTQYIICNVNHKFSNFKVDKRYEPKSCDPTHTCCPCPAP	234
Qy	260	ELLGGRSVLFPPEKRDLTMTSRPEVTCVYVDVSHEDPEVKFMVYDVGEVHNATKPR	319
Dd	235	ELLGGRSVLFPPEKRDLTMTSRPEVTCVYVDVSHEDPEVKFMVYDVGEVHNATKPR	294
Qy	320	EEQYNSTYFVNSVLIVLYLHODMLNGEYCKSKVSNKALRALPIEKTLSKAGQPREPOYYTLR	379
Dd	295	EEQYASTYFVNSVLIVLYLHODMLNGEYCKSKVSNKALRALPIEKTLSKAGQPREPOYYTLR	354
Qy	380	PSREEMTKNOVSLTCLVKGFPYSDIAVEMESNGCPENNNYKTTTPVLDSGGSFFLYSKLTV	439
Dd	355	PSHDELTKNOVSLTCLVKGFPYSDIAVEMESNGCPENNNYKTTTPVLDSGGSFFLYSKLTV	414
Qy	440	DKSRMOQGVNFCSVNHEALHNHTOKSLTSLSPK	474
Dd	415	DKSRMOQGVNFCSVNHEALHNHTOKSLTSLSPK	449

RESULT 4

IS-09-822-698A-26



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; Sequence 26, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MOCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DXX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 26
; LENGTH: 451
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Immunoglobulin heavy chain of MUC1-specific PH1-19G1
US-09-822-698A-26

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Query Match      89.8%; Score 2257; DB 10; Length 451;
Best Local Similarity 93.2%; Pred. No. 1.6e-147;
Matches 428; Conservative 7; Mismatches 12; Indels 12; Gaps 2;

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QY 20 EVOLLESGGLVOPGSLRLSCAASGFTFSNYSAMSVNQAPKGLKLEWVAISASGHTYL 79
   1 QVQLVQSGGGLVOPGSLRLSCAASGFTFRSNAMGVNQAPKGLEWVAISGSGSTYY 60
QY 80 ADVSKGRFTISRDNKNTLYLQMNSLRADETAVYYCAKDRVYTMVLNLGG---FDYWG 135
   61 ADVSKGRFTISRDNKNTLYLQMNSLRADETAVYYCAK-----TGGVWDPIDYWG 112
DB 61 ADVSKGRFTISRDNKNTLYLQMNSLRADETAVYYCAK-----TGGVWDPIDYWG 112
QY 136 QGTRTVSASATKGPSPVPLAPSSKSTSGGTALGCLVKDYRPEPVYVSWNSGALTSGVH 195
   113 QGTRTVSASATKGPSPVPLAPSSKSTSGGTALGCLVKDYRPEPVYVSWNSGALTSGVH 172
DB 113 QGTRTVSASATKGPSPVPLAPSSKSTSGGTALGCLVKDYRPEPVYVSWNSGALTSGVH 172
QY 196 TFPYAVLOSSGLYSLSVYTPVSSSLGTQTYICNVNHNKPSNTVYDKRVRPKSCDKHTHCP 255
   173 TFPYAVLOSSGLYSLSVYTPVSSSLGTQTYICNVNHNKPSNTVYDKRVRPKSCDKHTHCP 232
DB 173 TFPYAVLOSSGLYSLSVYTPVSSSLGTQTYICNVNHNKPSNTVYDKRVRPKSCDKHTHCP 232
QY 256 CPAPRLGPGSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFMYVYDGEVHNNAK 315
   233 CPAPRLGPGSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFMYVYDGEVHNNAK 292
DB 233 CPAPRLGPGSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFMYVYDGEVHNNAK 292
QY 316 TKPREEQYNSTYRVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKGQPREPOV 375
   293 TKPREEQYNSTYRVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKGQPREPOV 352
DB 293 TKPREEQYNSTYRVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKGQPREPOV 352
QY 376 YTLPSREMTKKNQVSLCLVKGFPYSDIAVEMESNGQPENNYKTPPYLDSGSEFLYLS 435
   353 YTLPSREMTKKNQVSLCLVKGFPYSDIAVEMESNGQPENNYKTPPYLDSGSEFLYLS 412
DB 353 YTLPSREMTKKNQVSLCLVKGFPYSDIAVEMESNGQPENNYKTPPYLDSGSEFLYLS 412
QY 436 KLTVDKSRMQQGNVFSCSVMEHALHNHYTOKSLSPGK 474
   413 KLTVDKSRMQQGNVFSCSVMEHALHNHYTOKSLSPGK 451
DB 413 KLTVDKSRMQQGNVFSCSVMEHALHNHYTOKSLSPGK 451

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RESULT 5
US-10-150-475A-6

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; Sequence 6, Application US/10150475A
; Publication No. US20030103985A1
; GENERAL INFORMATION:
; APPLICANT: Adolff, G. et al.
; TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoc conjugates
; FILE REFERENCE: 1/1211
; CURRENT APPLICATION NUMBER: US/10/150,475A
; CURRENT FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: US 60/307,451
; PRIOR FILING DATE: 2001-07-24
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6

```

```

; LENGTH: 444
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Humanised
; OTHER INFORMATION: Murine Antibody B1W4 Heavy Chain SEQ ID NO: 6
US-10-150-475A-6

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Query Match      89.5%; Score 2249.5; DB 15; Length 444;
Best Local Similarity 92.7%; Pred. No. 5e-147;
Matches 422; Conservative 12; Mismatches 10; Indels 11; Gaps 1;

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QY 20 EVOLLESGGLVOPGSLRLSCAASGFTFSNYSAMSVNQAPKGLKLEWVAISASGHTYL 79
   1 EVOLLESGGLVOPGSLRLSCAASGFTFSNYSAMSVNQAPKGLKLEWVAISGSGSTYY 60
DB 1 EVOLLESGGLVOPGSLRLSCAASGFTFSNYSAMSVNQAPKGLKLEWVAISGSGSTYY 60
QY 80 ADVSKGRFTISRDNKNTLYLQMNSLRADETAVYYCAKDRVYTMVLNLGG---FDYWG 139
   61 ADVSKGRFTISRDNKNTLYLQMNSLRADETAVYYCAK-----GLDYWGKRTLL 109
DB 61 ADVSKGRFTISRDNKNTLYLQMNSLRADETAVYYCAK-----GLDYWGKRTLL 109
QY 140 VTVSSASTKGPSPVPLAPSSKSTSGGTALGCLVKDYRPEPVYVSWNSGALTSGVHPFPA 199
   110 VTVSSASTKGPSPVPLAPSSKSTSGGTALGCLVKDYRPEPVYVSWNSGALTSGVHPFPA 169
DB 110 VTVSSASTKGPSPVPLAPSSKSTSGGTALGCLVKDYRPEPVYVSWNSGALTSGVHPFPA 169
QY 200 VVQSSGLYSLSVYTPVSSSLGTQTYICNVNHNKPSNTVYDKRVRPKSCDKHTHCP 259
   170 VVQSSGLYSLSVYTPVSSSLGTQTYICNVNHNKPSNTVYDKRVRPKSCDKHTHCP 229
DB 170 VVQSSGLYSLSVYTPVSSSLGTQTYICNVNHNKPSNTVYDKRVRPKSCDKHTHCP 229
QY 260 ELIGGPGSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFMYVYDGEVHNNAKTKPR 319
   230 ELIGGPGSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFMYVYDGEVHNNAKTKPR 289
DB 230 ELIGGPGSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFMYVYDGEVHNNAKTKPR 289
QY 320 EEQYNSTYRVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTL 379
   290 EEQYNSTYRVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTL 349
DB 290 EEQYNSTYRVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTL 349
QY 380 PSREMTKKNQVSLCLVKGFPYSDIAVEMESNGQPENNYKTPPYLDSGSEFLYLSKLV 439
   350 PSREMTKKNQVSLCLVKGFPYSDIAVEMESNGQPENNYKTPPYLDSGSEFLYLSKLV 409
DB 350 PSREMTKKNQVSLCLVKGFPYSDIAVEMESNGQPENNYKTPPYLDSGSEFLYLSKLV 409
QY 440 DKSRMQGNVFSCSVMEHALHNHYTOKSLSPGK 474
   410 DKSRMQGNVFSCSVMEHALHNHYTOKSLSPGK 444
DB 410 DKSRMQGNVFSCSVMEHALHNHYTOKSLSPGK 444

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RESULT 6
US-10-020-786-9

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```

; Sequence 9, Application US/10020786
; Publication No. US20030073164A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Laura C.
; APPLICANT: Klimowski, Laura
; APPLICANT: Reilly, Dorothea
; APPLICANT: Yansura, Daniel G.
; TITLE OF INVENTION: PROKAROTICALLY PRODUCED ANTIBODIES AND USES THEREOF
; FILE REFERENCE: P1793R1
; CURRENT APPLICATION NUMBER: US/10/020,786
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/256,164
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 11
; SEQ ID NO 9
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: anti-IF heavy chain
US-10-020-786-9

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Query Match      87.4%; Score 2196; DB 15; Length 470;
Best Local Similarity 88.6%; Pred. No. 2.6e-143;
Matches 418; Conservative 9; Mismatches 37; Indels 8; Gaps 1;

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20 EVOLLESGGLVOPGSGRLSCAASGFETSNVAMSWROAPKGLWVSAISASHNYL 79  
1 EVOLVQSGGLVOPGSGRLSCAASGFETSNVAMSWROAPKGLWVSAISASHNYL 60  
80 ADVKGRFTISRDNSKNTLYLQNMNSLRADPVAVYCAKREVTMAIVLNGG--FDYMGOG 137  
61 NQFKRGRTLSRDNSKNTAYLQNMNSLRADPVAVYCAKREVTMAIVLNGG--FDYMGOG 115  
138 TRVYVSSASTKGPVFPPLAPSSKTSVGGTALGLVNDYFPPEVTVSNNSGALTSVHTF 197  
116 TLVYVSSASTKGPVFPPLAPSSKTSVGGTALGLVNDYFPPEVTVSNNSGALTSVHTF 175  
198 PAVLOSGGLYSLSSVYVTPSSSLGTOTYICVNHKPSNTKYDKRPEKSCDTHCCPCP 257  
176 PAVLOSGGLYSLSSVYVTPSSSLGTOTYICVNHKPSNTKYDKRPEKSCDTHCCPCP 235  
258 APPELLGSPVFLFPKPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGEVHNATK 317  
236 APPELLGSPVFLFPKPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGEVHNATK 295  
318 PREQYNTYRVSVYTLVHODWLNKKEYKCKVSKALPAPLEKTSKAKGQPREPOYTT 377  
296 PREQYNTYRVSVYTLVHODWLNKKEYKCKVSKALPAPLEKTSKAKGQPREPOYTT 355  
378 LPSPREEMTKNOVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTPPVLDSDGSFFLYSKL 437  
356 LPSPREEMTKNOVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTPPVLDSDGSFFLYSKL 415  
438 TVDKSRMQGNVFCSCVMHEALHNHYTQKSLSLSPGK 474  
416 TVDKSRMQGNVFCSCVMHEALHNHYTQKSLSLSPGK 452

## RESULT 9

US-10-020-786-11  
Sequence 11, Application US/10020786  
Publication No. US20030073164A1  
GENERAL INFORMATION:  
APPLICANT: Simmons, Laura C.  
APPLICANT: Klimowski, Laura  
APPLICANT: Reilly, Dorothea  
APPLICANT: Yansura, Daniel G.  
TITLE OF INVENTION: PROKARYOTICALLY PRODUCED ANTIBODIES AND USES THEREOF  
FILE REFERENCE: P1793R1  
CURRENT APPLICATION NUMBER: US/10/020,786  
CURRENT FILING DATE: 2002-03-26  
PRIOR APPLICATION NUMBER: US 60/256,164  
PRIOR FILING DATE: 2000-12-14  
NUMBER OF SEQ ID NOS: 11  
SEQ ID NO 11  
LENGTH: 476  
TYPE: PRT  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: anti-VEGF heavy chain  
US-10-020-786-11

Query Match 87.0%; Score 2187; DB 15; Length 476;  
Best Local Similarity 88.8%; Pred. No. 1.1e-142;  
Matches 420; Conservative 14; Mismatches 35; Indels 4; Gaps 3;  
3 FGLSMFLVAILKGVQCEVOLLESGGLVOPGSGRLSCAASGFETSNVAMSWROAPK 62  
7 FLASMFVFIATNAYAVLVEGSGGLVOPGSGRLSCAASGFETSNVAMSWROAPK 66  
63 GLEWVSAISA-SGHTYLAADVSKGRTISRDNSKNTLYLQNMNSLRADPVAVYCAKREVT 121  
67 GLEWVSAISA-SGHTYLAADVSKGRTISRDNSKNTLYLQNMNSLRADPVAVYCAKREVT 123  
122 TMIVLVNGFDYMGOGTRVYVSSASTKGPVFPPLAPSSKTSVGGTALGLVNDYFPPEV 181  
124 YVYGTSHMYFDYMGOGTRVYVSSASTKGPVFPPLAPSSKTSVGGTALGLVNDYFPPEV 183

162 TVSNMNSGALTSVHTFPAPVLOSGGLYSLSSVYVTPSSSLGTOTYICVNHKPSNTKYDKR 241  
164 TVSNMNSGALTSVHTFPAPVLOSGGLYSLSSVYVTPSSSLGTOTYICVNHKPSNTKYDKR 243  
242 VEPKSCDTHCCPCPAPPELLGSPVFLFPKPKDPTLMISRTPEVTCVVVDVSHEDPEVK 301  
244 VEPKSCDTHCCPCPAPPELLGSPVFLFPKPKDPTLMISRTPEVTCVVVDVSHEDPEVK 303  
302 FNMVYDGEVHNATKPREQYNTYRVSVYTLVHODWLNKKEYKCKVSKALPAPLEK 361  
304 FNMVYDGEVHNATKPREQYNTYRVSVYTLVHODWLNKKEYKCKVSKALPAPLEK 363  
362 TISKAKGQPREQYNTYRVSVYTLVHODWLNKKEYKCKVSKALPAPLEK 421  
364 TISKAKGQPREQYNTYRVSVYTLVHODWLNKKEYKCKVSKALPAPLEK 423  
422 PPVLDSDGSFFLYSKLTVDKSRMQGNVFCSCVMHEALHNHYTQKSLSLSPGK 474  
424 PPVLDSDGSFFLYSKLTVDKSRMQGNVFCSCVMHEALHNHYTQKSLSLSPGK 476

## RESULT 10

US-09-948-429B-8  
Sequence 8, Application US/09948429B  
Patent No. US20020177689A1  
GENERAL INFORMATION:  
APPLICANT: Anderson, Darrell R.  
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC TO HUMAN B7.1 AND/OR B7.2 PRIVATIZED FORMS THEREOF, PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS IMMUNOSUPPRESSANTS"  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BURNS, DOANE, SWECKER & MATHEIS  
STREET: 699 Prince Street  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22314  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.3C  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/948,429B  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/363,916  
FILING DATE:  
APPLICATION NUMBER: US 08/487,550  
FILING DATE: 07-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Teskin, Robin L.  
REGISTRATION NUMBER: 35,030  
REFERENCE/DOCKET NUMBER: 012712-131  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-836-6620  
TELEFAX: 703-836-2021  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 478 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-948-429B-8

Query Match 86.8%; Score 2183; DB 10; Length 478;  
Best Local Similarity 86.7%; Pred. No. 2.1e-142;  
Matches 418; Conservative 18; Mismatches 34; Indels 12; Gaps 3;  
1 MERGLSMFLVAILKGVQCEVOLLESGGLVOPGSGRLSCAASGFETSNVAMSWROAP 60

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01 1M6MSLLELVAVATRVGCEVQLVSGSGGLVQCGSLRVCANVSGCFLFSDHYMMFMFRAP 60
02 61 G6GLEVVSAI--SAGSHSTYLDVSGRGFTISDNKSNLTYLXOMNSIARBDYAVYCAKD 118
03 61 G6GPEWVGFIIRNKPNGTTEYAAVSVDRTISRDDSKSIAYLOWSSKIEDTAYVYCT-- 118
04 119 REVTMIVLVNGG-----FDYMGQGTIRVTYSSASTKGPSEVPEPLAPSSKSTSGGTAAGCL 172
05 119 --TSYISHRGVCYCIGYFEFQMGQALVTVSSASTKGPSPFPLAPSSKSTSGTAAGCL 176
06 173 VKDYFEPEVTVSNMNSGALTSGVHTFPFAVLQSSGLYSVYTVVPSSLGOTYICNVNHK 232
07 177 VVDYFEPEVTVSNMNSGALTSGVHTFPFAVLQSSGLYSVYTVVPSSLGOTYICNVNHK 236
08 223 PENTVKDKRVEPKSCOKTHCPPCPAPBELLGGSVFLFPPKPDOTLMSRPEVTCVVD 292
09 237 PENTKAYDKAEPKSCOKTHCPPCPAPBELLGGSVFLFPPKPDOTLMSRPEVTCVVD 296
10 293 VSHDEPEVKNMNVYDGEVHNNAKTBPREDQYNSTRVSVLTVLHDQMLNGEKVKCKYVN 352
11 297 VSHDEPEVKNMNVYDGEVHNNAKTBPREDQYNSTRVSVLTVLHDQMLNGEKVKCKYVN 356
12 353 KALPAPIETTSKAKQPREPOVYTLPRPSEEMTKNOVSLTCLYKGYPSDIAVEMWSNG 412
13 357 KALPAPIETTSKAKQPREPOVYTLPRPSEEMTKNOVSLTCLYKGYPSDIAVEMWSNG 416
14 413 QPENNKYTPPVLDSDSGSEFLYSKLTIVDKSRMOGQNFSCSVMHAEALHNHYTOKSLSP 472
15 417 QPENNKYTPPVLDSDSGSEFLYSKLTIVDKSRMOGQNFSCSVMHAEALHNHYTOKSLSP 476
16 473 GK 474
17 477 GK 478
18
19 RESULT 11
20 US-10-124-807-8
21 Sequence 8, Application US/10124807
22 Publication No. US20030166207A1
23 GENERAL INFORMATION:
24 APPLICANT: Anderson, Darrell R.
25 TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
26 TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF.
27 TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
28 TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
29 NUMBER OF SEQUENCES: 12
30 CORRESPONDENCE ADDRESS:
31 ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
32 STREET: 699 Prince Street
33 CITY: Alexandria
34 STATE: VA
35 COUNTRY: USA
36 ZIP: 22314
37 COMPUTER READABLE FORM:
38 MEDIUM TYPE: Floppy disk
39 COMPUTER: IBM PC compatible
40 OPERATING SYSTEM: PC-DOS/MS-DOS
41 SOFTWARE: PatentIn Release #1.0, Version #1.30
42 CURRENT APPLICATION DATA:
43 APPLICATION NUMBER: US/10/124,807
44 FILING DATE:
45 CLASSIFICATION:
46 PRIOR APPLICATION DATA:
47 APPLICATION NUMBER: 09/383,916
48 FILING DATE:
49 APPLICATION NUMBER: US 08/487,550
50 FILING DATE: 07-JUN-1995
51 ATTORNEY/AGENT INFORMATION:
52 NAME: Teskin, Robin L.
53 REGISTRATION NUMBER: 35,030
54 REFERENCE/DOCKET NUMBER: 012712-131
55 TELECOMMUNICATION INFORMATION:

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: TELEPHONE: 703-836-6620
: TELEFAX: 703-836-2021
: INFORMATION FOR SEQ ID NO: 8:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 478 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-10-124-807-8

Query Match      86.8%; Score 2183; DB 12; Length 478;
Best Local Similarity 86.7%; Pred. No. 2,1e-142;
Matches 418; Conservative 18; Mismatches 34; Indels 12; Gaps 3;

      1 MEEGLSMFLPVALIKGVOCEVOILLESGGIVPGSGSLRLSCAASGTFPSNAMSVPAP 60
      1 MGGMLLEFLPVAATRQQCEVQLVESGGGLVQPGSSLRVSCAASGTFSDHMYFRRQAP 60
      61 GKGLEWYSAI--SASGHSYTLADSVKGRFTISDNKNTLYLQMNLSRAEDTAVYYCAKD 118
      61 GKGDEWVGFIIRNKNPGTGTEYLAASVKDRFTISNDSKSIAYLQMSLKLIEDTAVYYCT-- 118
      119 REVMYIVLVNGG-----FDYWGQGRVYVSSASTGSPVFPPLAPSSKTSGGTAAIGCL 172
      119 --TSYISHCRGGVCCYGGYFEFFWGGALVTVSSASTGSPVFPPLAPSSKTSGGTAAIGCL 176
      173 VKDFFPPPVYVSNMNSGALITSGVHTPPAVLQSSGLTSLSSVWYVPSSSLTQTYICNVNHK 232
      177 VKQDFPPPVYVSNMNSGALITSGVHTFPRAVLQSSGLTSLSSVWYVPSSSLQTYITICNVNHK 236
      233 PSNTKVDKRVKPKSCDTHTCPPCAPPELLGGSVFLPPPKPKDTLMISRTPDEVTCVVD 292
      237 PSNTKVDKRVKPKSCDTHTCPPCAPPELLGGSVFLPPPKPKDTLMISRTPDEVTCVVD 296
      293 VSHEDPVRKRWNVVDGVEVHNAAKTRPREQVNSTYRVVSVLTLYLHODWLVNGEKYCKVSN 352
      297 VSHEDPVRKRWNVVDGVEVHNAAKTRPREQVNSTYRVVSVLTLYLHODWLVNGEKYCKVSN 356
      353 KALPAPIEKTISRAGQPREPOVYTLPPSHEETKNQVSLTCLVKGFPSPDIAVEMESNG 412
      357 KALPAPIEKTISRAGQPREPOVYTLPPSHEETKNQVSLTCLVKGFPSPDIAVEMESNG 416
      413 QPENNYKTPPEVLDSOSFFLYSKLVNDSRMQGGVYFCSYVNEALHNHYTKSLSLSP 472
      417 QPENNYKTPPEVLDSOSFFLYSKLVNDSRMQGGVYFCSYVNEALHNHYTKSLSLSP 476
      QY      473 GK 474
      477 GK 478

RESULT 12
US-10-124-905-8
: Sequence 8, Application US/10124905
: Publication No. US2002016136A1
: GENERAL INFORMATION:
: APPLICANT: Anderson, Darrell R.
: TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
: TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
: TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
: TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
: NUMBER OF SEQUENCES: 12
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: BURNS, DOANE, SWECKER & MATHIAS
: STREET: 699 Prince Street
: CITY: Alexandria
: STATE: VA
: COUNTRY: USA
: ZIP: 22314
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/124,905
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/383,916
; FILING DATE:
; APPLICATION NUMBER: US 08/487,550
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-10-124-905-8

Query Match      86.8%; Score 2183; DB 14; Length 478;
Best Local Similarity 86.7%; Pred. No. 2.1e-142;
Matches 418; Conservative 18; Mismatches 34; Indels 12; Gaps 3;

Oy 1 MEFGLSMFLVAIIKVOCEVQLLESGLVOPGSGSLRLSCAASGFTFSNYAMSVMVROAP 60
Db 1 MGLMILLFLVAIVATRVQCEVQLVESGGGLVOPGSGSLVSCAVSFETSDHMYFROAP 60
Oy 61 GKGLEWVAI--SASGHSYLADEVKGRFTISRDNSKNTLYIQMNSLRADETAVYYCAK 118
Db 61 GKGEMWGFIRNKPNGGTFTEYAAVSKDRFTISRDSKSIAYLQMSLSLKIEDTAVYYCT-- 118
Oy 119 REVMIIVLVNGG-----FDYWGQGRVTVSSASTKGPSVFPLAASSKSTSGTAALGL 172
Db 119 --TSTISHRGVGYCYGFERWGOGLVTVSSASTKGPSVFPLAASSKSTSGTAALGL 176
Oy 173 VKDYFPEPVTVSMNSGALTSGVHPFPAVLQSSGLYSLSSVVPSSSLGTQTYICNVNHK 232
Db 177 VKDYFPEPVTVSMNSGALTSGVHTFPAVLQSSGLYSLSSVVPSSSLGTQTYICNVNHK 236
Oy 233 PSNTRKVDKRVKSCDKTHCTCPCPAPPELLGGPSVFLPPTPKKDTLMISTRPEVTCVVD 292
Db 237 PSNTRKVDKAEPRKSCDKTHCTCPCPAPPELLGGPSVFLPPTPKKDTLMISTRPEVTCVVD 296
Oy 293 VSHEDPEVKFMYVDGVENVNAKTRPREQYNSTYRVYSVLTVLDHQMILNGEKYCKYSN 352
Db 297 VSHEDPEVKFMYVDGVENVNAKTRPREQYNSTYRVYSVLTVLDHQMILNGEKYCKYSN 356
Oy 353 KALPAPIKITSKAKGQPREPOVYTLPPSRREEMTKNOVSLTCLVKGFYPSDIAVEMESNG 412
Db 357 KALPAPIKITSKAKGQPREPOVYTLPPSRREEMTKNOVSLTCLVKGFYPSDIAVEMESNG 416
Oy 413 QPENNYKTTTPVLDSGSEFLYSLKLVDSKRWQOGNVFSCSYMHDLAHNHYTQKSLSLSP 472
Db 417 QPENNYKTTTPVLDSGSEFLYSLKLVDSKRWQOGNVFSCSYMHDLAHNHYTQKSLSLSP 476
Oy 473 GK 474
Db 477 GK 478

RESULT 13
US-10-356-974-2
; Sequence 2, Application US/10356974
; Publication No. US20030153735A1
; GENERAL INFORMATION:
; APPLICANT: BRECE, TIMOTHY N.
; APPLICANT: FAHRNER, ROBERT L.
```

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; APPLICANT: GORRELL, JEFFREY R.
; APPLICANT: PHAM LAZARESCI, KATHLYN
; APPLICANT: LESTER, PHILIP M.
; APPLICANT: PENG, DAVID
; TITLE OF INVENTION: PROTEIN PURIFICATION
; FILE REFERENCE: P1939R1
; CURRENT APPLICATION NUMBER: US/10/356,974
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: US 60/354,579
; PRIOR FILING DATE: 2002-02-05
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 2
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized.
; US-10-356-974-2

Query Match      86.8%; Score 2181.5; DB 12; Length 449;
Best Local Similarity 90.6%; Pred. No. 2.4e-142;
Matches 416; Conservative 8; Mismatches 20; Indels 15; Gaps 2;

Oy 20 EYQLLESGLVOPGSGSLRLSCAASGFTFSNYAMSVMVROAPGKGLEWVAISASGHSYLA 79
Db 1 EYQLVESGGGLVOPGSGSLRLSCAASGFNINKDVIYIHVYRQAPGKGLEWVAIRIYPTNGYTRY 60
Oy 80 ADSVKGRTFISRDNSKNTLYIQMNSLRADETAVYYCAKDR YTMIVLVNGG-----FDYW 134
Db 61 ADSVKGRTFISADTSKNTAYLQMSLSLRADETAVYYCSR-----WGCGGFYAMDYV 110
Oy 135 GGGRTVTVSSASTKGPSVFPLAAPSSTSGGTAALGLCYKYPEPEPVTVSMNSGALTSGV 194
Db 111 GGGTLVTVSSASTKGPSVFPLAAPSSTSGGTAALGLCYKYPEPEPVTVSMNSGALTSGV 170
Oy 195 HTPFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPS NTRKVDKRVKSCDKTHCTCP 254
Db 171 HTPFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPS NTRKVDKRVKSCDKTHCTCP 230
Oy 255 PCPAPPELLGGPSVFLPPTPKKDTLMISTRPEVTCVVDVS HEDPEVKFMYVDGVENVNA 314
Db 231 PCPAPPELLGGPSVFLPPTPKKDTLMISTRPEVTCVVDVS HEDPEVKFMYVDGVENVNA 290
Oy 315 KTRPREQYNSTYRVYSVLTVLDHQMILNGEKYCKYSNKA LAPAPIKITSKAKGQPREQ 374
Db 291 KTRPREQYNSTYRVYSVLTVLDHQMILNGEKYCKYSNKA LAPAPIKITSKAKGQPREQ 350
Oy 375 VYTPPSPREEMTKNOVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTTPVLDSGSEFLY 434
Db 351 VYTPPSPREEMTKNOVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTTPVLDSGSEFLY 410
Oy 435 SKLVDSKRWQOGNVFSCSYMHDLAHNHYTQKSLSPG 173
Db 411 SKLVDSKRWQOGNVFSCSYMHDLAHNHYTQKSLSPG 149

RESULT 14
US-10-253-366-2
; Sequence 2, Application US/10253366
; Publication No. US20030078388A1
; GENERAL INFORMATION:
; APPLICANT: BASEY, CAROL D.
; APPLICANT: BLANK, GREG S.
; TITLE OF INVENTION: PROTEIN PURIFICATION
; FILE REFERENCE: P1241R1
; CURRENT APPLICATION NUMBER: US/10/253,366
; CURRENT FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: US/09/304,465
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 2
; LENGTH: 449
; TYPE: PRT
```

ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: Sequence is synthesized.  
US-10-253-366-2

Query Match 86.8%; Score 2181.5; DB 15; Length 449;  
Best Local Similarity 90.6%; Pred. No. 2.4e-142;  
Matches 416; Conservative 8; Mismatches 20; Indels 15; Gaps -2;

```
QY 20 EVOLLESGGGLVPGGSLRLSCAASGFTFSNVAWSVROAPGKLEWVSATISAGHSTYL 79
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EVOLVESGGGLVPGGSLRLSCAASGFTFSNVAWSVROAPGKLEWVSATISAGHSTYL 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 80 ADVSKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKREVTMIIVLNGG----FDYW 134
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ADVSKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCSR-----WGCDGFYAMDYW 110
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 135 GGGTRVYSSASTGSPVFLPAPSSKSTSGGTALGCLVKDYFPEPTVSNNSGALTSGV 194
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 111 GGGTLVYVSSASTGSPVFLPAPSSKSTSGGTALGCLVKDYFPEPTVSNNSGALTSGV 170
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 195 HTFPAVLQSSGLYSLSSVYTPSPSSLTGQTYICNVNHPSTNTKYDKRVEPKCDKTHTCP 254
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 171 HTFPAVLQSSGLYSLSSVYTPSPSSLTGQTYICNVNHPSTNTKYDKRVEPKCDKTHTCP 230
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 255 PCPAPELLGSPVFLFPKPKDGLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGEVYHNA 314
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 231 PCPAPELLGSPVFLFPKPKDGLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGEVYHNA 290
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 315 KTKPREQYNSTYRVSVLTVYLHODMVLNGKRYKCKVSKKALPAPIEKTISKAKGQPRRPQ 374
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 291 KTKPREQYNSTYRVSVLTVYLHODMVLNGKRYKCKVSKKALPAPIEKTISKAKGQPRRPQ 350
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 375 VYTLPPSRREEMTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPRPVLDSDGSFELY 434
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 351 VYTLPPSRREEMTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPRPVLDSDGSFELY 410
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 435 SKLTVDKSRMQQGNVFSCSVNHEALHNHYTQKSLSLSPG 473
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 411 SKLTVDKSRMQQGNVFSCSVNHEALHNHYTQKSLSLSPG 449
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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RESULT 15  
US-10-316-694-2  
Sequence 2, Application US/10316694  
Publication No. US20030118583A1  
GENERAL INFORMATION:  
APPLICANT: EMERY, JEFFERSON C.  
APPLICANT: MCDONALD, PAUL J.  
APPLICANT: O'LEARY, RHONA M.  
TITLE OF INVENTION: STABILIZING POLYPEPTIDES WHICH HAVE BEEN EXPOSED TO UREA  
FILE REFERENCE: P1940R1  
CURRENT APPLICATION NUMBER: US/10/316,694  
CURRENT FILING DATE: 2002-12-11  
PRIOR APPLICATION NUMBER: US 60/341,891  
PRIOR FILING DATE: 2001-12-19  
NUMBER OF SEQ ID NOS: 2  
SEQ ID NO 2  
LENGTH: 449  
TYPE: PRT  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: Sequence is synthesized.  
US-10-316-694-2

Query Match 86.8%; Score 2181.5; DB 15; Length 449;  
Best Local Similarity 90.6%; Pred. No. 2.4e-142;  
Matches 416; Conservative 8; Mismatches 20; Indels 15; Gaps 2;

```
QY 20 EVOLLESGGGLVPGGSLRLSCAASGFTFSNVAWSVROAPGKLEWVSATISAGHSTYL 79
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EVOLVESGGGLVPGGSLRLSCAASGFTFSNVAWSVROAPGKLEWVSATISAGHSTYL 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

```
QY 80 ADVSKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKREVTMIIVLNGG----FDYW 134
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ADVSKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCSR-----WGCDGFYAMDYW 110
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 135 GGGTRVYSSASTGSPVFLPAPSSKSTSGGTALGCLVKDYFPEPTVSNNSGALTSGV 194
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 111 GGGTLVYVSSASTGSPVFLPAPSSKSTSGGTALGCLVKDYFPEPTVSNNSGALTSGV 170
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 195 HTFPAVLQSSGLYSLSSVYTPSPSSLTGQTYICNVNHPSTNTKYDKRVEPKCDKTHTCP 254
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 171 HTFPAVLQSSGLYSLSSVYTPSPSSLTGQTYICNVNHPSTNTKYDKRVEPKCDKTHTCP 230
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 255 PCPAPELLGSPVFLFPKPKDGLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGEVYHNA 314
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 231 PCPAPELLGSPVFLFPKPKDGLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGEVYHNA 290
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 315 KTKPREQYNSTYRVSVLTVYLHODMVLNGKRYKCKVSKKALPAPIEKTISKAKGQPRRPQ 374
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 291 KTKPREQYNSTYRVSVLTVYLHODMVLNGKRYKCKVSKKALPAPIEKTISKAKGQPRRPQ 350
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 375 VYTLPPSRREEMTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPRPVLDSDGSFELY 434
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 351 VYTLPPSRREEMTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPRPVLDSDGSFELY 410
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 435 SKLTVDKSRMQQGNVFSCSVNHEALHNHYTQKSLSLSPG 473
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 411 SKLTVDKSRMQQGNVFSCSVNHEALHNHYTQKSLSLSPG 449
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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Search completed: September 12, 2003, 13:06:06  
Job time : 32.7966 secs

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RESULT 1
AA014066
ID   AA014066 standard; Protein; 234 AA.
XX
AC   AA014066;
XX
DT   07-MAY-2002 (first entry)
XX
DE   Light chain protein of the monoclonal antibody from clone JA.
XX
KW   HRG; human rabies-immune globulin; monoclonal; virucide; heavy chain;
KM   human monoclonal rabies virus neutralising antibody; immunoglobulin;
XX   light chain; central nervous system; CNS; prophylactic therapy; clone JA.
XX
OS   Homo sapiens.
XX
WO20018132-A2.
XX
PN
PD   22-NOV-2001.
XX
PF   04-MAY-2001; 2001WO-US14468.
XX
PR   16-MAY-2000; 2000US-204518P.
XX
PA   (UYJE-) UNIV JEFFERSON THOMAS.
XX
PI   Hooper DC, Dietzschold B;
XX
PT   WPI: 2002-062381/08.
DR   N-PSDB; AAK98702.
XX
PT   Novel isolated human monoclonal rabies virus neutralising antibody
XX

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```

FT Modified-site 72 /note= "potential protein kinase C phosphorylation site"
FT Modified-site 87 /note= "potential casein kinase II phosphorylation site"
FT Modified-site 96 /note= "potential casein kinase II phosphorylation site"
FT Modified-site 122 /note= "potential casein kinase II phosphorylation site"
FT Modified-site 147..216 /note= "potential casein kinase II phosphorylation site"
FT Domain /label= immunoglobulin_domain
FT Domain /label= immunoglobulin
FT Modified-site 182 /note= "immunoglobulin"
FT Modified-site 184 /note= "potential casein kinase II phosphorylation site"
FT Modified-site 190..233 /note= "potential casein kinase II phosphorylation site"
FT Domain /label= signature_sequence
FT Modified-site 202 /note= "immunoglobulin"
FT Domain /note= "potential casein kinase II phosphorylation site"
FT Domain 212..229 /label= signature_sequence
FT Domain /note= "immunoglobulin"
XX MO200020588-A2.
XX 13-APR-2000.
XX 01-OCT-1999; 99WO-US22908.
XX 02-OCT-1998; 98US-0165621.
XX (INCY-) INCYTE PHARM INC.
XX Tang YF, Corley NC, Guegler KJ, Lu DAM;
XX MPI: 2000-303775/26.
XX N-PSDB: AAA09154.
XX Purified polypeptide for treating or preventing disorders associated
XX with decreased expression or activity of bone marrow-derived serum
XX proteins
XX Claim 1; Page 68-69; 72pp; English.
XX Human bone marrow-derived serum proteins (BMDSP) 1 has chemical and
XX structural similarity with immunoglobulin kappa light chain. BMDSP-1
XX and BMDSP-2 are useful for treating or preventing a disorder associated
XX with decreased expression or activity of BMDSP.
XX Antagonists of BMDSP are useful for treating or preventing a disorder
XX associated with increased expression or activity of bone marrow-derived
XX serum proteins. The disorders include cancers (melanoma, adenocarcinoma,
XX sarcoma), immune disorders (acquired immunodeficiency syndrome (AIDS),
XX asthma, atherosclerosis, Crohn's disease, bronchitis, multiple sclerosis,
XX osteo- and rheumatoid arthritis), viral infections, parasitic infections,
XX schistosoma, tapeworm), and vascular disorders (arteriosclerosis,
XX hypertension, vasculitis).
XX Sequence 234 AA:
SQ
Query Match 92.5%; Score 1131; DB 21; Length 234;
Best Local Similarity 92.7%; Pred. No. 3,6e-64;
Matches 217; Conservative 7; Mismatches 10; Indels 0; Gaps 0;
OY 1 MEAPQQLFLLLMLPDTGETIVLQSPATLSLSPGERATLACRASQTSRYLAWYQQR 60
DB 1 MEAPQQLFLLLMLPDTGETIVLQSPATLSLSPGERATLACRASQTSRYLAWYQQR 60
OY 61 GQAPRLLYIVDSNRATGIPARFSGSGGTDFLTLSLSEPEDFAVYCCQQRNWPWFQ 120
DB 61 GQAPRLLYIVDSNRATGIPARFSGSGGTDFLTLSLSEPEDFAVYCCQQRNWPWFQ 120

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OY 121 GTRKEFRNVAAAPSVIFPPSPDQLKSGTASVYCLLNFEYIPRAKVQMKVDNALQSGNSQ 180
DB 121 GTRLEKRRVAAAPSVIFPPSPDQLKSGTASVYCLLNFEYIPRAKVQMKVDNALQSGNSQ 180
OY 181 ESVTEGDSKDSYTSLSSTLTLSKADYKKRVACEVTHOGJSSPVTKSFNRGEC 234
DB 181 ESVTEGDSKDSYTSLSSTLTLSKADYKKRVACEVTHOGJSSPVTKSFNRGEC 234
RESULT 4
AAG71272
AAG71272 standard; Protein; 236 AA.
AC AAG71272;
XX 30-JUL-2001 (first entry)
XX Human gene 2-encoded secreted protein HTSER67, SEQ ID NO:121.
XX Human: secreted protein; proliferative disorder; cancer; chromosome 1;
XX foetal abnormality; developmental abnormality; haematopoietic disorder;
XX immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
XX inflammation; allergy; neurological disorder; Alzheimer's disease;
XX Parkinson's disease; cognitive disorder; schizophrenia; asthma;
XX skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;
XX cardiovascular disorder; angiotensin disorder; kidney disorder;
XX gastrointestinal disorder; pregnancy-related disorder; tumour;
XX endocrine disorder; infection; wound healing; vulnery;
XX cell culture; chemotaxis; food additive;
XX binding partner identification.
XX Homo sapiens.
XX WO200132674-A1.
XX 10-MAY-2001.
XX 25-OCT-2000; 2000WO-US29360.
XX 29-OCT-1999; 99US-0162211.
XX 30-JUN-2000; 2000US-0215138.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Ruben SM, Komatsoulis GA, Young PE, Moore PA;
XX MPI: 2001-291051/30.
XX N-PSDB: AAH31379.
XX New nucleic acid molecule encoding a human secreted protein, useful for
XX preventing, treating or ameliorating medical conditions such as
XX rheumatoid arthritis, Alzheimer's disease and microbial infections -
XX Claim 11; Page 498-499; 581pp; English.
XX AAH31349-AAH31428 represent cDNAs corresponding to 26 human secreted
XX protein genes, and AAG71243-AAG71319 represent the proteins they encode.
XX AAG71320-AAG71403 represent human secreted protein fragments. The genes
XX and their corresponding secreted proteins are useful for preventing,
XX treating or ameliorating medical conditions, e.g., by protein or gene
XX therapy. Pathological conditions can be diagnosed by determining the
XX amount of the new protein in a sample or by determining the presence of
XX mutations in the new genes. Specific uses are described for each of the
XX 52 genes, based on the tissues in which they are most highly expressed,
XX and include developing products for the diagnosis or treatment of
XX proliferative disorders, cancer, tumours, foetal and developmental
XX abnormalities, haematopoietic disorders, diseases of the immune system,
XX AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation,
XX allergies, neurological disorders (e.g., Alzheimer's disease,
XX Parkinson's disease), cognitive disorders, schizophrenia, asthma,
XX skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis,
XX cardiovascular disorders, angiogenic disorders, kidney disorders,

```

CC gastrointestinal disorders, pregnancy-related disorders, endocrine  
 CC disorders, and infections. The proteins can also be used to aid wound  
 CC healing and epithelial cell proliferation, to prevent skin aging due to  
 CC sunburn, to maintain organs before transplantation, for supporting cell  
 CC culture of primary tissues, to regenerate tissues, to identify their  
 CC cognate ligands or binding partners, and in chemotaxis, and can be used  
 CC as a food additive or preservative to modify storage properties.  
 CC Antibodies specific for a protein of the invention can be used in  
 CC alleviating symptoms associated with the disorders mentioned above, and  
 CC in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked  
 CC immunoassort assay (ELISA). The present sequence represents a human  
 CC secreted protein of the invention.

XX Sequence 236 AA;

Query Match 92.3%; Score 1129; DB 22; Length 236;

Best Local Similarity 92.4%; Pred. No. 4.8e-64;

Matches 218; Conservative 4; Mismatches 12; Indels 2; Gaps 1;

DB 1 MEPAQLFLLLMLPDTTGEIVLTQSPATLSLSPGERATLACRASQTSRYLAWYQOKP 60  
 1 MEXPAQLFLLLMLPDTTGEIVLTQSPATLSLSPGERATLACRASQTSRYLAWYQOKP 60

OY 61 GOAPRLIYDTSNRATGIPARFSGSGSTDEFTLSTISLPEDEFAVYCOQRFNMP--WTF 118  
 61 GOAPRLIYXASXRATGIPARFSGSGSTDEFTLSTISLPEDEFAVYCOQRFNMP--WTF 120

OY 119 GOGTVEKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQMKVDNALQSGN 178  
 121 GXGTVETKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQMKVDNALQSGN 180

OY 179 SOESTVEDSKDSTYSLSTLTLSKADYEKKHVACEVTHQGLSSPYKSNRREGC 234  
 181 SOESTVEDSKDSTYSLSTLTLSKADYEKKHVACEVTHQGLSSPYKSNRREGC 236

RESULT 5  
 ABG63490  
 ID ABG63490 standard; Protein: 236 AA.

XX ABG63490;

DT 27-AUG-2002 (first entry)

DE Human albumin fusion protein #165.

KW Albumin fusion protein; therapeutic protein X; human albumin; HA;  
 KW human serum albumin; HSA; cancer; reproductive disorder;  
 KW digestive disorder; immune disorder; endocrine disorder;  
 KW haematopoietic disorder; neural disorder; connective disorder;  
 KW cytosolic; antiniferility; antiinflammatory; antitumor;  
 KW immunomodulator; anti-HIV; antidiabetic; haemostatic; nootropic;  
 KW osteopathic; antiparkinsonian; antimicrobial; neuroleptic;  
 KW osteopathic; antichrilitic.

XX Homo sapiens.  
 OS Synthetic.

XX WO200177137-A1.

PD 18-OCT-2001.

PF 12-APR-2001; 2001WO-US11988.

PR 12-APR-2000; 2000US-229358P.

PR 25-APR-2000; 2000US-199384P.

PR 21-DEC-2000; 2000US-256931P.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Rosen CA, Haseltine WA;

DR WPI: 2002-010886/01.

XX New fusion protein for treating disease e.g. diabetes comprises an  
 PT albumin fused to a therapeutic protein -  
 PS Claim 1; Page 682; 2102pp; English.

XX The present invention relates to albumin fusion proteins comprising a  
 CC therapeutic protein X and human albumin (HA, also known as human serum  
 CC albumin, HSA). The proteins are useful for treating a disease or  
 CC disorder that may be modulated by therapeutic protein X. The albumin  
 CC extends the shelf-life of protein X, and may increase its biological  
 CC in vitro/in vivo activity. The protein is useful for treating and  
 CC diagnosing disorders such as cancer, reproductive disorders, digestive  
 CC disorders (e.g. Crohn's disease, ulcerative colitis), immune disorders  
 CC (e.g. acquired immunodeficiency syndrome, AIDS), endocrine disorders  
 CC (e.g. diabetes), haematopoietic disorders, neural disorders  
 CC (e.g. Alzheimer's, Parkinson's, Creutzfeldt-Jacob disease,  
 CC encephalomyelitis, meningitis, schizophrenia), and connective disorders  
 CC (e.g. osteoporosis, arthritis). ABG63326-ABG65518 represent albumin  
 CC fusion proteins of the invention.

XX Sequence 236 AA;

Query Match 92.3%; Score 1129; DB 23; Length 236;

Best Local Similarity 92.4%; Pred. No. 4.8e-64;

Matches 218; Conservative 4; Mismatches 12; Indels 2; Gaps 1;

OY 1 MEPAQLFLLLMLPDTTGEIVLTQSPATLSLSPGERATLACRASQTSRYLAWYQOKP 60  
 1 MEXPAQLFLLLMLPDTTGEIVLTQSPATLSLSPGERATLACRASQTSRYLAWYQOKP 60

OY 61 GOAPRLIYDTSNRATGIPARFSGSGSTDEFTLSTISLPEDEFAVYCOQRFNMP--WTF 118  
 61 GOAPRLIYXASXRATGIPARFSGSGSTDEFTLSTISLPEDEFAVYCOQRFNMP--WTF 120

OY 119 GOGTVEKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQMKVDNALQSGN 178  
 121 GXGTVETKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQMKVDNALQSGN 180

OY 179 SOESTVEDSKDSTYSLSTLTLSKADYEKKHVACEVTHQGLSSPYKSNRREGC 234  
 181 SOESTVEDSKDSTYSLSTLTLSKADYEKKHVACEVTHQGLSSPYKSNRREGC 236

RESULT 6  
 AAY93702  
 ID AAY93702 standard; Protein: 235 AA.

XX AAY93702;

DT 03-OCT-2000 (first entry)

DE The kappa chain of immunoglobulin clone 4.1.1.

KW Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system;  
 KW hyperimmunity disorder; autoimmune disease; diabetes; graft rejection;  
 KW proliferative disorder; cancer; immunodeficient disorder.

XX Homo sapiens.

PN WO200037504-A2.

PD 29-JUN-2000.

PF 23-DEC-1999; 99WO-US30895.

PR 23-DEC-1998; 98US-0113647.

PA (PFIZ ) PFIZER INC.

PA (ABGE-) ABGENIX INC.

PI Hanson DC, Neveu MJ, Mueller EE, Hanke JH, Gilman SC, Davis CG;  
 Corvalan JR;

XX MPI: 2000-442647/38.  
 DR N-PSDB: AAA46865.  
 XX  
 PT Novel antibodies capable of binding cytotoxic T-lymphocyte antigen  
 PT (CTLA)-4 containing specified heavy and light chain sequences, useful  
 PT for treating, e.g. immune disorders -  
 XX  
 PS Claim 3; Fig 1A; 157pp; English.  
 XX  
 CC The present sequence represents a kappa chain of an antibody of the  
 CC invention. The antibody is directed cytotoxic T-lymphocyte antigen  
 CC (CTLA)-4. Antibodies of the invention are composed of a heavy chain  
 CC variable region, comprising a modified contiguous sequence from a  
 CC FR1-FR3 sequence encoded by a human VH3-33 family gene. The  
 CC modifications are contained in CDR1, CDR2 and/or framework regions.  
 CC The antibodies may be used to inhibit CTLA-4 and down-regulate the  
 CC immune system to treat hyperimmunity disorders (e.g. autoimmune  
 CC disease, diabetes and graft rejection) and proliferative disorders  
 CC (e.g. cancer). CTLA-4 stimulatory agents may be used to up-regulate  
 CC immune system to up-regulate immunodeficient disorders.  
 CC  
 XX Sequence 235 AA:  
 SQ  
 Query Match 90.6%; Score 1108.5; DB 21; Length 235;  
 Best Local Similarity 91.5%; Pred. No. 9.5e-63;  
 Matches 215; Conservative 7; Mismatches 12; Indels 1; Gaps 1;  
 QY 1 MEAPQQLFLLLMLPDTGTEIVLTQSPATLSLSPGERATLACRASQT-ASRYLAWYQK 59  
 Db 1 METPAQLFLLLMLPDTGTEIVLTQSPGTLISLSPGERATLSCRASQSISSFLAWYQQR 60  
 QY 60 PGQAPRLIYDTSNRATGIPARFSGSGGTPTLTSSLEPEDPAVYVCCQGFNMPFTFG 119  
 Db 61 PGQAPRLIYDTSNRATGIPARFSGSGGTPTLTSSLEPEDPAVYVCCQGFNMPFTFG 120  
 QY 120 QGTKEFERVTAAPSVFIFPPSDDEQLKSGTASVCLNNFYPREAKVOMKVDNALQSGNS 179  
 Db 121 QGTKEIERKRYTAAPSVFIFPPSDDEQLKSGTASVCLNNFYPREAKVOMKVDNALQSGNS 180  
 QY 180 QESVTEODSKDSTVSLSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 234  
 Db 181 QESVTEODSKDSTVSLSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 235

RESULT 7  
 AAY93729  
 ID AAY93729 standard; Protein: 235 AA.  
 XX  
 AC AAY93729;  
 XX  
 DT 03-OCT-2000 (first entry)  
 XX  
 DE The kappa chain of immunoglobulin clone 4.1.1.  
 XX  
 KW Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system;  
 KW hyperimmunity disorder; autoimmune disease; diabetes; graft rejection;  
 KW proliferative disorder; cancer; immunodeficient disorder.  
 XX  
 OS Homo sapiens.  
 XX  
 FT Key Location/Qualifiers  
 FT Peptide 1..20 /note= "signal peptide"  
 XX  
 PN WO200037504-A2.  
 XX  
 PD 29-JUN-2000.  
 XX  
 PF 23-DEC-1999; 99WO-US30895.  
 XX  
 PR 23-DEC-1998; 98US-0113647.  
 XX

PA (Pfiz ) PFIZER INC.  
 PA (ABGE-) ABGENIX INC.  
 XX  
 PI Hanson DC, Neveu MJ, Mueller EE, Hanke JH, Gilman SC, Davis CG;  
 PI Corvaelan JR;  
 XX  
 DR MPI: 2000-442647/38.  
 DR N-PSDB: AAA46893.  
 XX  
 PT Novel antibodies capable of binding cytotoxic T-lymphocyte antigen  
 PT (CTLA)-4 containing specified heavy and light chain sequences, useful  
 PT for treating, e.g. immune disorders -  
 XX  
 PS Claim 3; Fig 22g; 157pp; English.  
 XX  
 CC The present sequence represents a kappa chain of an antibody of the  
 CC invention. The antibody is directed cytotoxic T-lymphocyte antigen  
 CC (CTLA)-4. Antibodies of the invention are composed of a heavy chain  
 CC variable region, comprising a modified contiguous sequence from a  
 CC FR1-FR3 sequence encoded by a human VH3-33 family gene. The  
 CC modifications are contained in CDR1, CDR2 and/or framework regions.  
 CC The antibodies may be used to inhibit CTLA-4 and down-regulate the  
 CC immune system to treat hyperimmunity disorders (e.g. autoimmune  
 CC disease, diabetes and graft rejection) and proliferative disorders  
 CC (e.g. cancer). CTLA-4 stimulatory agents may be used to up-regulate  
 CC immune system to up-regulate immunodeficient disorders.  
 CC  
 XX Sequence 235 AA:  
 SQ  
 Query Match 90.6%; Score 1108.5; DB 21; Length 235;  
 Best Local Similarity 91.5%; Pred. No. 9.5e-63;  
 Matches 215; Conservative 7; Mismatches 12; Indels 1; Gaps 1;  
 QY 1 MEAPQQLFLLLMLPDTGTEIVLTQSPATLSLSPGERATLACRASQT-ASRYLAWYQK 59  
 Db 1 METPAQLFLLLMLPDTGTEIVLTQSPGTLISLSPGERATLSCRASQSISSFLAWYQQR 60  
 QY 60 PGQAPRLIYDTSNRATGIPARFSGSGGTPTLTSSLEPEDPAVYVCCQGFNMPFTFG 119  
 Db 61 PGQAPRLIYDTSNRATGIPARFSGSGGTPTLTSSLEPEDPAVYVCCQGFNMPFTFG 120  
 QY 120 QGTKEFERVTAAPSVFIFPPSDDEQLKSGTASVCLNNFYPREAKVOMKVDNALQSGNS 179  
 Db 121 QGTKEIERKRYTAAPSVFIFPPSDDEQLKSGTASVCLNNFYPREAKVOMKVDNALQSGNS 180  
 QY 180 QESVTEODSKDSTVSLSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 234  
 Db 181 QESVTEODSKDSTVSLSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 235

RESULT 8  
 ABP71366  
 ID ABP71366 standard; Protein: 235 AA.  
 XX  
 AC ABP71366;  
 XX  
 DT 28-APR-2003 (first entry)  
 XX  
 DE Anti-OPGL-1 antibody kappa light chain.  
 XX  
 KW Osteoprotegerin ligand; osteopathic; antiinflammatory; antirheumatic;  
 KW antirheumatic; cytostatic; OPGL; anti-OPGL-1; antibody.  
 XX  
 OS Mus musculus.  
 XX  
 FT Key Location/Qualifiers  
 FT Peptide 1..20 /note= "IgG2 signal peptide"  
 FT Region 21..128 /note= "variable region"  
 FT Region 129..235 /note= "constant region"  
 XX

PN WO2003002713-A2.  
XX 09-JAN-2003.  
PD 25-JUN-2002; 2002WO-US20181.  
XX 26-JUN-2001; 2001US-301172P.  
XX (ABGE-) ABGENIX INC.  
PA (AMGE-) AMGEN INC.  
XX Boyle WJ, Martin RH, Corvalan JR, Davis GC;  
PI WPI: 2003-210262/20.  
DR N-PSDB: AB259148.  
XX  
XX New antibodies that interact with osteoprotegerin ligands, useful for  
PT treating osteopenic disorders, e.g. osteoporosis, bone loss from  
PT arthritis, Paget's disease, osteopenia, osteomyelitis, hypercalcemia  
PT and osteonecrosis -  
XX  
XX Claim 1; Fig 4; 144pp; English.  
PS  
XX The invention relates to antibodies that interact with osteoprotegerin  
CC ligands (OPG). The antibody is useful for detecting the level of OPG in  
CC a biological sample. The antibody, or the pharmaceutical composition  
CC comprising the antibody, is also useful for treating osteopenic disorder,  
CC an inflammatory condition with attendant bone loss, an autoimmune  
CC condition with attendant bone loss in a patient or rheumatoid arthritis  
CC in a patient. In particular, the antibody or composition is useful for  
CC treating bone diseases, e.g. osteoporosis, bone loss from arthritis,  
CC Paget's disease, osteopenia, endocrine osteoporosis (e.g. Cushing's  
CC syndrome or acromegaly), osteogenesis imperfecta, homocystinuria,  
CC McKusick syndrome, Riley-Day syndrome, osteomyelitis, hypercalcemia, or  
CC osteonecrosis. The present sequence represents an anti-OPG-1 antibody  
CC kappa light chain.  
XX  
XX Sequence 235 AA:  
SQ  
Query Match 89.9%; Score 1099.5; DB 24; Length 235;  
Best Local Similarity 91.5%; Pred. No. 3.5e-62;  
Matches 215; Conservative 6; Mismatches 13; Indels 1; Gaps 1;  
QY 1 MEAPQALLFLLLMLPPTTGIEIVLTQSPATLSLSPGERATLACRASQTA-SRYLAWYQOK 59  
Db 1 MEAPQALLFLLLMLPPTTGIEIVLTQSPATLSLSPGERATLACRASQTA-SRYLAWYQOK 60  
QY 60 PGQAPRLIYDTSNRATGIPARFSGSGGTDFLTISISLEPEDFAVYYCQGRFNMPTFG 119  
Db 61 PGQAPRLIYDTSNRATGIPARFSGSGGTDFLTISISLEPEDFAVYYCQGRFNMPTFG 120  
QY 120 QGTVEFKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKYQMKVDNALQSGNS 179  
Db 121 QGTVEFKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKYQMKVDNALQSGNS 180  
QY 180 QESTVEDSKDSTYSLSTLTLSKADYEKKHKKVACEVTHQGLSSPVTKSFNRGEC 234  
Db 181 QESTVEDSKDSTYSLSTLTLSKADYEKKHKKVACEVTHQGLSSPVTKSFNRGEC 235

RESULT 9  
AAV93708  
ID AAV93708 standard; Protein: 234 AA.  
XX  
XX AAV93708;  
XX  
XX 03-OCT-2000 (first entry)  
XX  
XX The kappa chain of immunoglobulin clone 6.1.1.  
XX  
XX Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system;  
KM hyperimmune disorder; autoimmune disease; diabetes; graft rejection;  
KW proliferative disorder; cancer; immunodeficient disorder.

XX Homo sapiens.  
OS  
XX WO200037504-A2.  
XX  
XX 29-JUN-2000.  
PD 23-DEC-1999; 99WO-US30895.  
XX 23-DEC-1998; 98US-0113647.  
XX  
XX (PRIZ ) PRIZER INC.  
PA (ABGE-) ABGENIX INC.  
XX  
XX Hanson DC, Neveu MJ, Mueller EE, Hanke JH, Gilman SC, Davis CG;  
PI Corvalan JR;  
XX  
XX WPI: 2000-442647/38.  
DR N-PSDB: AAA46871.  
XX  
XX Novel antibodies capable of binding cytotoxic T-lymphocyte antigen  
PT (CTLA)-4 containing specified heavy and light chain sequences, useful  
PT for treating, e.g. immune disorders -  
XX  
XX  
XX Claim 3; Fig 1D; 157pp; English.  
PS  
XX The present sequence represents a kappa chain of an antibody of the  
CC invention. The antibody is directed cytotoxic T-lymphocyte antigen  
CC (CTLA)-4. Antibodies of the invention are composed of a heavy chain  
CC variable region, comprising a modified contiguous sequence from a  
CC FRI-FR3 sequence encoded by a human VH3-33 family gene. The  
CC modifications are contained in CDRI, CDR2 and/or framework regions.  
CC The antibodies may be used to inhibit CTLA-4 and down-regulate the  
CC immune system to treat hyperimmune disorders (e.g. autoimmune  
CC disease, diabetes and graft rejection) and proliferative disorders  
CC (e.g. cancer). CTLA-4 stimulatory agents may be used to up-regulate  
CC immune system to up-regulate immunodeficient disorders.  
XX  
XX Sequence 234 AA:  
SQ  
Query Match 89.6%; Score 1096; DB 21; Length 234;  
Best Local Similarity 91.0%; Pred. No. 5.8e-62;  
Matches 213; Conservative 6; Mismatches 15; Indels 0; Gaps 0;  
QY 1 MEAPQALLFLLLMLPPTTGIEIVLTQSPATLSLSPGERATLACRASQTA-SRYLAWYQOK 60  
Db 1 MEAPQALLFLLLMLPPTTGIEIVLTQSPATLSLSPGERATLACRASQTA-SRYLAWYQOK 60  
QY 61 GOAPRLIYDTSNRATGIPARFSGSGGTDFLTISISLEPEDFAVYYCQGRFNMPTFG 120  
Db 61 GOAPRLIYDTSNRATGIPARFSGSGGTDFLTISISLEPEDFAVYYCQGRFNMPTFG 120  
QY 121 GTRVEFKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKYQMKVDNALQSGNS 180  
Db 121 GTRVEFKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKYQMKVDNALQSGNS 180  
QY 181 ESYTEODSKDSTYSLSTLTLSKADYEKKHKKVACEVTHQGLSSPVTKSFNRGEC 234  
Db 181 ESYTEODSKDSTYSLSTLTLSKADYEKKHKKVACEVTHQGLSSPVTKSFNRGEC 234

RESULT 10  
AAV93733  
ID AAV93733 standard; Protein: 234 AA.  
XX  
XX AAV93733;  
XX  
XX 03-OCT-2000 (first entry)  
XX  
XX The kappa chain of immunoglobulin clone 6.1.1.  
XX  
XX Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system;  
KM hyperimmunity disorder; autoimmune disease; diabetes; graft rejection;  
KW

KW proliferative disorder; cancer; immunodeficient disorder.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..20  
 XX /note= "signal peptide"  
 XX  
 PN WO200037504-A2.  
 XX  
 PD 29-JUN-2000.  
 XX  
 PF 23-DEC-1999; 99WO-US30895.  
 XX  
 PR 23-DEC-1998; 98US-0113647.  
 XX  
 PA (PF12 ) PEIZER INC.  
 XX (ABGE-) ABGENIX INC.  
 XX  
 PI Hanson DC, Neveu MJ, Mueller EE, Hanke JH, Gilman SC, Davis CG,  
 PI Corvalan JR;  
 XX  
 DR WPI: 2000-442647/38.  
 DR N-PSDB; AAA46897.  
 XX  
 PT Novel antibodies capable of binding cytotoxic T-lymphocyte antigen  
 PT (CTLA)-4 containing, specified heavy and light chain sequences, useful  
 PT for treating, e.g. immune disorders -  
 XX  
 PS Claim 3; Fig 22o; 157pp; English.  
 XX  
 CC The present sequence represents a kappa chain of an antibody of the  
 CC invention. The antibody is directed cytotoxic T-lymphocyte antigen  
 CC (CTLA)-4. Antibodies of the invention are composed of a heavy chain  
 CC variable region, comprising a modified contiguous sequence from a  
 CC FRI-FR3 sequence encoded by a human VH3-33 family gene. The  
 CC modifications are contained in CDRI, CDRI2 and/or framework regions.  
 CC The antibodies may be used to inhibit CTLA-4 and down-regulate the  
 CC immune system to treat hyperimmunity disorders (e.g. autoimmune  
 CC disease, diabetes and graft rejection) and proliferative disorders  
 CC (e.g. cancer). CTLA-4 stimulatory agents may be used to up-regulate  
 CC immune system to up-regulate immunodeficient disorders.  
 CC  
 XX  
 SQ Sequence 234 AA:  
 Query Match 89.6%; Score 1096; DB 21; Length 234;  
 Best Local Similarity 91.0%; Pred. No. 5,8e-62;  
 Matches 213; Conservative 6; Mismatches 15; Indels 0; Gaps 0;  
 QY 1 MEAPQQLFLLLMLPDTTGEIVLTQSPATLSLGERATLACRASQTSRLIAYQOKP 60  
 DB 1 MEAPQQLFLLLMLPDTTGEIVLTQSPATLSLGERATLACRASQTSRLIAYQOKP 60  
 QY 61 GOAPRLIYDTNRAITGIPARFSGSGGTFTLSSLEPEDFAVYVCOQRNMPWTFQ 120  
 DB 61 GOAPRLIYDVSSRAITGIPDRFSGSGGTFTLITSLRLEPEDFAVYVCOQGISPTTGP 120  
 QY 121 GTKVEFKRTVAAPSVFIFPPSDEQLKSGTASVVCCLINFFPREAKVQWKVDNALGSGNSQ 180  
 DB 121 GTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLINFFPREAKVQWKVDNALGSGNSQ 180  
 QY 181 ESYTEODSKDSTYSLSSTITLTKADYEKHKVYACEVTHOGLSSPYTKSPNRGEC 234  
 DB 181 ESYTEODSKDSTYSLSSTITLTKADYEKHKVYACEVTHOGLSSPYTKSPNRGEC 234

DT 27-OCT-1994 (first entry)  
 XX  
 DE Human anti-IgE MAb light chain.  
 XX  
 KW Human IgE; CH4 region; triggers mediator release;  
 KW Mast cells; Monoclonal antibody; allergy.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Region 21..128  
 XX /label= light chain variable region  
 XX  
 PN EP592230-A1.  
 XX  
 PD 13-APR-1994.  
 XX  
 PF 07-OCT-1993; 93EP-0308006.  
 XX  
 PR 07-OCT-1992; 92JP-0293800.  
 XX  
 PA (SNOW ) SNOW BRAND MILK PROD CO LTD.  
 XX  
 PI Goto M, Kobayashi F, Mizuno A, Morinaga T, Washida N;  
 PI Yoshida T;  
 XX  
 DR WPI: 1994-120330/15.  
 DR N-PSDB; AAQ71872.  
 XX  
 PT Human monoclonal anti-IgE peptide antibody - inhibits histamine  
 PT release from mast cells by allergen stimulation, useful for  
 PT preventing allergies  
 XX  
 PS Claim 3; Page 12; 21pp; English.  
 XX  
 CC AAR52951 shows the light chain of a human type anti-IgE peptide  
 CC monoclonal antibody which inhibits the signal transmission for  
 CC the release of chemical mediator from mast cells and basophils  
 CC stimulated with allergen. The antibody can be used for the  
 CC prophylaxis and the therapy of allergy.  
 CC (updated on 25-MAR-2003 to correct PN field.)  
 CC  
 XX  
 SQ Sequence 234 AA:  
 Query Match 89.1%; Score 1090; DB 15; Length 234;  
 Best Local Similarity 89.3%; Pred. No. 1,4e-61;  
 Matches 209; Conservative 10; Mismatches 15; Indels 0; Gaps 0;  
 QY 1 MEAPQQLFLLLMLPDTTGEIVLTQSPATLSLGERATLACRASQTSRLIAYQOKP 60  
 DB 1 MEAPQQLFLLLMLPDTTGEIVLTQSPATLSVPGRAALCRASQTSNNIAYQOKP 60  
 QY 61 GOAPRLIYDTNRAITGIPARFSGSGGTFTLSSLEPEDFAVYVCOQRNMPWTFQ 120  
 DB 61 AOAAPRLIYGTATGATGIPARFSGSGGTFTLITSLSDFAIYVCOQYSMPWTFQ 120  
 QY 121 GTKVEFKRTVAAPSVFIFPPSDEQLKSGTASVVCCLINFFPREAKVQWKVDNALGSGNSQ 180  
 DB 121 GTKVDLKGTVAAAPSVFIFPPSDEQLKSGTASVVCCLINFFPREAKVQWKVDNALGSGNSQ 180  
 QY 181 ESYTEODSKDSTYSLSSTITLTKADYEKHKVYACEVTHOGLSSPYTKSPNRGEC 234  
 DB 181 ESYTEODSKDSTYSLSSTITLTKADYEKHKVYACEVTHOGLSSPYTKSPNRGEC 234

## RESULT 11

AAR52951  
 ID AAR52951 standard; Protein; 234 AA.  
 XX  
 AC AAR52951;  
 XX  
 DT 25-MAR-2003 (updated)

## RESULT 12

AAY93704  
 ID AAY93704 standard; Protein; 233 AA.  
 XX  
 AC AAY93704;  
 XX  
 DT 03-OCT-2000 (first entry)

DE The kappa chain of immunoglobulin clone 4.8.1.  
 XX Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system;  
 XX hyperimmunity disorder; autoimmune disease; diabetes; graft rejection;  
 KW proliferative disorder; cancer; immunodeficient disorder.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200037504-A2.  
 XX  
 PD 29-JUN-2000.  
 XX  
 PD 23-DEC-1999; 99WO-US30895.  
 XX  
 PR 23-DEC-1998; 98US-0113647.  
 XX  
 PA (Pfizer) Pfizer Inc.  
 XX (ABGE-) ABGENIX INC.  
 XX  
 PI Hanson DC, Neveu MJ, Mueller EE, Hanke JH, Gilman SC, Davis CG;  
 PI Corvalan JR;  
 XX  
 DR MPI: 2000-442647/38.  
 DR N-PSDB: AAA46867.  
 XX  
 PT Novel antibodies capable of binding cytotoxic T-lymphocyte antigen  
 PT (CTLA)-4 containing specified heavy and light chain sequences, useful  
 PT for treating, e.g. immune disorders -  
 XX  
 PS Claim 3; Fig 1B; 157pp; English.  
 XX  
 CC The present sequence represents a kappa chain of an antibody of the  
 CC invention. The antibody is directed cytotoxic T-lymphocyte antigen  
 CC (CTLA)-4. Antibodies of the invention are composed of a heavy chain  
 CC variable region, comprising a modified contiguous sequence from a  
 CC FRI-FR3 sequence encoded by a human VH3-33 family gene. The  
 CC modifications are contained in CDR1, CDR2 and/or framework regions.  
 CC The antibodies may be used to inhibit CTLA-4 and down-regulate the  
 CC immune system to treat hyperimmunity disorders (e.g. autoimmune  
 CC disease, diabetes and graft rejection) and proliferative disorders  
 CC (e.g. cancer). CTLA-4 stimulatory agents may be used to up-regulate  
 CC immune system to up-regulate immunodeficient disorders.  
 CC  
 XX  
 SQ Sequence 233 AA;  
 Query Match 88.8%; Score 1085.5; DB 21; Length 233;  
 Best Local Similarity 91.0%; Pred. No. 2.7e-61;  
 Matches 213; Conservative 5; Mismatches 15; Indels 1; Gaps 1;  
 Oy 1 MEAPAQLLFLLMLPDTTGEIVLTQSPATLSLSPGERATLACRASQTASRYLAWYQOKP 60  
 Db 1 METPAQLLFLLMLPDTTGEIVLTQSPGTLSPGERATLSCRTS-VSSSYLAWYQOKP 59  
 Oy 61 GOAPRLLIYDTSNRATGIPARFSGSGSTDEFTLSTISLEPPDFAVYYCOQRFNMPPTGG 120  
 Db 60 GOAPRLLIYGASNRATGIPDRFSGSGSTDEFTLTISLEPPDFAVYYCOQYGISPTTGG 119  
 Oy 121 GTKVEFKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVNALQSGNSQ 180  
 Db 120 GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVNALQSGNSQ 179  
 Oy 181 ESVTEQDSKSTYSLSSTLTLSKADYEKHKYVACEVTHQGLSSPVTSSFNNGEC 234  
 Db 180 ESVTEQDSKSTYSLSSTLTLSKADYEKHKYVACEVTHQGLSSPVTSSFNNGEC 233  
 RESULT 13  
 AAY93731  
 ID AAY93731 standard; Protein; 233 AA.  
 XX  
 AC AAY93731;  
 XX  
 DT 03-OCT-2000 (first entry)

XX  
 DE The kappa chain of immunoglobulin clone 4.8.1.  
 XX Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system;  
 KW hyperimmunity disorder; autoimmune disease; diabetes; graft rejection;  
 KW proliferative disorder; cancer; immunodeficient disorder.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200037504-A2.  
 XX  
 PD 29-JUN-2000.  
 XX  
 PD 23-DEC-1999; 99WO-US30895.  
 XX  
 PR 23-DEC-1998; 98US-0113647.  
 XX  
 PA (Pfizer) Pfizer Inc.  
 XX (ABGE-) ABGENIX INC.  
 XX  
 PI Hanson DC, Neveu MJ, Mueller EE, Hanke JH, Gilman SC, Davis CG;  
 PI Corvalan JR;  
 XX  
 DR MPI: 2000-442647/38.  
 DR N-PSDB: AAA46895.  
 XX  
 PT Novel antibodies capable of binding cytotoxic T-lymphocyte antigen  
 PT (CTLA)-4 containing specified heavy and light chain sequences, useful  
 PT for treating, e.g. immune disorders -  
 XX  
 PS Claim 3; Fig 22k; 157pp; English.  
 XX  
 CC The present sequence represents a kappa chain of an antibody of the  
 CC invention. The antibody is directed cytotoxic T-lymphocyte antigen  
 CC (CTLA)-4. Antibodies of the invention are composed of a heavy chain  
 CC variable region, comprising a modified contiguous sequence from a  
 CC FRI-FR3 sequence encoded by a human VH3-33 family gene. The  
 CC modifications are contained in CDR1, CDR2 and/or framework regions.  
 CC The antibodies may be used to inhibit CTLA-4 and down-regulate the  
 CC immune system to treat hyperimmunity disorders (e.g. autoimmune  
 CC disease, diabetes and graft rejection) and proliferative disorders  
 CC (e.g. cancer). CTLA-4 stimulatory agents may be used to up-regulate  
 CC immune system to up-regulate immunodeficient disorders.  
 CC  
 XX  
 SQ Sequence 233 AA;  
 Query Match 88.8%; Score 1085.5; DB 21; Length 233;  
 Best Local Similarity 91.0%; Pred. No. 2.7e-61;  
 Matches 213; Conservative 5; Mismatches 15; Indels 1; Gaps 1;  
 Oy 1 MEAPAQLLFLLMLPDTTGEIVLTQSPATLSLSPGERATLACRASQTASRYLAWYQOKP 60  
 Db 1 METPAQLLFLLMLPDTTGEIVLTQSPGTLSPGERATLSCRTS-VSSSYLAWYQOKP 59  
 Oy 61 GOAPRLLIYDTSNRATGIPARFSGSGSTDEFTLSTISLEPPDFAVYYCOQRFNMPPTGG 120  
 Db 60 GOAPRLLIYGASNRATGIPDRFSGSGSTDEFTLTISLEPPDFAVYYCOQYGISPTTGG 119  
 Oy 121 GTKVEFKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVNALQSGNSQ 180  
 Db 120 GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVNALQSGNSQ 179  
 Oy 181 ESVTEQDSKSTYSLSSTLTLSKADYEKHKYVACEVTHQGLSSPVTSSFNNGEC 234  
 Db 180 ESVTEQDSKSTYSLSSTLTLSKADYEKHKYVACEVTHQGLSSPVTSSFNNGEC 233  
 RESULT 14  
 AAR12128

ID	AARL2128 standard; Protein: 349 AA.
XX	
AC	AARL2128;
XX	
DT	25-MAR-2003 (updated)
DT	01-AUG-1991 (first entry)
DE	1B1 IgG aberrant light chain with duplicated variable region.
XX	
KM	immunoglobulin G; light chain; variable region; duplication;
KM	passive immunity; group B streptococci.
XX	
OS	Homo sapiens.
XX	
FH	Key Location/Qualifiers
FT	Peptide 1..17
FT	/label= leader peptide
FT	Region 18..130
FT	/label= variable region
FT	/note= "L'V 1"
FT	Region 131..243
FT	/label= variable region
FT	/note= "L'V 2"
FT	Region 244..345
FT	/label= constant region
XX	
PN	WO9106305-A.
XX	
PD	16-MAY-1991.
XX	
PX	06-NOV-1990; 90WO-USO6426.
XX	
PR	07-NOV-1989; 89US-O432700.
XX	
PA	(BRIM ) BRISTOL-MYERS SQUIBB CO.
PI	Shuford WM, Harris LJ, Rafi HV;
XX	
DR	WPI: 1991-163947/22.
DR	N-PSDB: AAO11878.
XX	
PT	Oligomeric immunoglobulin(s) with high avidity for antigen(s) -
PT	formed by duplicating esp. variable region of light chain of IgG
PT	class
XX	
PS	Example 5; Fig 16; 104pp; English.
XX	
CC	This sequence is deduced from the cDNA clone 4B9-VK15 and includes
CC	the amino acid sequence beyond the first stop codon. The clone is
CC	incomplete, starting from the G of the ATG initiator codon, but the
CC	initial Met is given. Antibody molecules of the invention can
CC	include one or two aberrant light chains containing a duplicated
CC	variable region, to produce heavier antibodies. These heavier
CC	antibodies were found to have higher avidity than antibodies with
CC	just a single copy of the L/V region. The antibodies can be used to
CC	treat disease, e.g. infection by Streptococcus agalactiae. They are
CC	able to pass across the placenta.
CC	See also AAO11879 and AAO11880.
CC	(Updated on 25-MAR-2003 to correct PA field.)
XX	
SQ	Sequence 349 AA;
Query Match	88.5%; Score 1082.5; DB 12; Length 349;
Best Local Similarity	63.6%; Pred. No. 6e-61;
Matches 222; Conservative 3; Mismatches 9; Indels 115; Gaps 2	
Dd	1 MEADPAQLLELLMLPDTTGEIVLTQSPTSLSPEGERATLACRASQTASRYLAHYQQKP 60       1 MEADPAQLLELLMLPDTTGEIVLTQSPTSLSPEGERATLSCRASQSGSYLAHYQQKP 60 
Dy	61 GOAERLLIYDTSNATGTGPARESSGSSTDTTLISSLEPEDFANYTCQQRNP----- 115       61 GOAERPLLYDSNATGTGPARESSGSTDFTLITSSLEPEDFAVYYCOHRDNMPGATE 120 

QY	116	-----	115
Db	121	GGGKFKVEIKHTGEIVLTOSPATLSLSPGERATLSCRASQ;VGSYLAWYQOKPQOABRPL	180
QY	116	-----	125
Db	181	ITYDASNATGCIIPARFSSGSGCTDFTLTITSSLEPEDFAVY;QHRDNNPFGATFGCGTKVE	240
QY	126	FKRTVAAPSVFIFPPESDOLKSGTAYVCLINNFYPREAKYOMKVDNALQSGNSQESVTE	185
Db	241	IKRTVAAPSVFIFPPESDOLKSGTAYVCLINNFYPREAKYOMKVDNALQSGNSQESVTE	300
QY	186	QDSKDSYSLSSSTLTLSKADYEKKRYVACEYTHOGLSSPVKSKNRECC	234
Db	301	QDSKDSYSLSSSTLTLSKADYEKKRYVACEYTHOGLSSPVKSKNRECC	349
RESULT 15			
AA13111	AA13111	standard; Protein; 414 AA.	
XX	AA13111;		
XX	AC		
XX	25-MAR-2003 (updated)		
DT	01-AUG-1991 (first entry)		
XX	1B1	196 aberrant light chain with duplicated variable region.	
XX	immunoglobulin G; light chain; variable region; duplication;		
KW	passive immunity; group B streptococci.		
XX	Homo sapiens.		
OS			
XX	Key	Location/Qualifiers	
FX	Peptide	1..17	
FT	Region	/label= leader peptide	
FT	Region	18..130	
FT	Region	/label= variable region	
FT	Region	/note= "L/V 1"	
FT	Region	131..243	
FT	Region	/label= variable region	
FT	Region	/note= "L/V 2"	
FT	Region	244..345	
FT	Region	/label= constant region	
XX	WO9106305-A.		
PN	16-MAY-1991.		
XX			
PD	06-NOV-1990;	90WO-US06426.	
XX			
PF	07-NOV-1989;	89US-0432700.	
PR			
XX	(BRIM ) BRISTOL-MYERS SQUIBB CO.		
PA			
XX	Shuford WM, Harris LJ, Raff HV;		
PI			
XX	WPI; 1991-163947/22.		
DR	N-PSDB; AAQ11878.		
XX			
PT	Oligomeric immunoglobulin(s) with high avidity for antigen(s) -		
PT	formed by duplicating esp. variable region of light chain of IgG		
PT	class		
XX			
XX	Example 5; Fig 16; 104pp; English.		
PS			
XX			
CC	This sequence is deduced from the cDNA clone 4B9-VK15 and includes		
CC	the amino acid sequence beyond the first stop codon ("x" in the		
CC	sequence represents a nonsense codon). The clone is incomplete,		
CC	starting from the G of the ATG initiator codon, but the initial Met		
CC	is given. Antibody molecules of the invention can include one or two		
CC	aberrant light chains containing a duplicated variable region, to		

CC produce heavier antibodies. These heavier antibodies were found to  
 CC have higher avidity than antibodies with just a single copy of the  
 CC L/V region. The antibodies can be used to treat disease, e.g.  
 CC infection by streptococcus agalactiae. They are able to pass across  
 CC the placenta.  
 CC See also AAQ11879 and AAQ11880.  
 CC (Updated on 25-MAR-2003 to correct PA field.)  
 CC  
 XX

SQ Sequence 414 AA:

Query Match 88.5%: Score 1082.5: DB 12: Length 414;  
 Best Local Similarity 63.6%: Pred. No. 7.1e-61;  
 Matches 222: Conservative 3: Mismatches 9: Indels 115: Gaps 2;

```

QY 1 MEAPQLLELLMLPDTGELVLTQSPATLSLSPGERATLACRASQTSRYLAMYQOKP 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 MEAPQLLELLMLPDTGELVLTQSPATLSLSPGERATLACRASQTSRYLAMYQOKP 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 61 GOAPRLIYDTSNRATGIPARFSGSGSTDTLTLSISLEPEDFAVYCCQGRPNP---- 115
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 GOAPRLIYDTSNRATGIPARFSGSGSTDTLTLSISLEPEDFAVYCCQGRPNP----- 120
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 116 ----- 115
Db 121 GGGTVEIKHTTGEIVLTQSPATLSLSPGERATLSCRASQSVSYLAMYQOKPGQAPRPL 180
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 116 -----TFGGTKVE 125
Db 181 IYDASNRATGIPARFSGSGSTDTLTLSISLEPEDFAVYCCQGRPNP----- 240
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 126 EKRTVAAPSVFIFPPSDEQLKSGTASVYCLNNFYPREAKYQWKVDNALQSGNSQESVTE 185
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 241 IKRTVAAPSVFIFPPSDEQLKSGTASVYCLNNFYPREAKYQWKVDNALQSGNSQESVTE 300
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 186 QDSKSTYSLSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 234
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 301 QDSKSTYSLSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 349
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
  
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Search completed: September 12, 2003, 13:00:41  
 Job time : 41.9915 secs



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## OM protein - protein search, using sw model

Run on: September 12, 2003, 12:58:39 ; Search time 26.7797 Seconds  
(without alignments)  
748.902 Million cell updates/sec

Title: US-09-848-832-3  
Perfect score: 2514  
Sequence: 1 MEGLSWLFLVAILKGVC.....MHEALNHHTQKSLSPGK 474

Scoring table: BIOSUM62  
Gapop 10.0 , Gapect 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PTUS.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/Backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2221.5	88.4	459	1	US-08-157-101A-7 Sequence 7, Appl
2	2193.5	87.3	452	3	US-09-027-449-71 Sequence 71, Appl
3	2193.5	87.3	452	3	US-09-026-985-71 Sequence 71, Appl
4	2193.5	87.3	452	4	US-09-121-952A-71 Sequence 71, Appl
5	2193.5	87.3	452	4	US-09-234-340A-71 Sequence 71, Appl
6	2183	86.8	478	3	US-08-487-550-8 Sequence 8, Appl
7	2183	86.8	478	4	US-09-526-098-8 Sequence 8, Appl
8	2181.5	86.8	449	4	US-09-679-397-2 Sequence 2, Appl
9	2181.5	86.8	449	4	US-09-680-148-2 Sequence 2, Appl
10	2181.5	86.8	449	4	US-09-304-465A-2 Sequence 2, Appl
11	2178	86.6	453	3	US-08-466-151-8 Sequence 8, Appl
12	2178	86.6	453	4	US-08-466-151-8 Sequence 8, Appl
13	2173	86.4	451	2	US-08-887-352B-18 Sequence 18, Appl
14	2173	86.4	451	3	US-09-109-207C-18 Sequence 18, Appl
15	2173	86.4	451	3	US-09-282-505-2 Sequence 2, Appl
16	2173	86.4	451	3	US-09-054-255-2 Sequence 2, Appl
17	2173	86.4	451	3	US-09-296-005-18 Sequence 18, Appl
18	2173	86.4	451	4	US-09-282-846-2 Sequence 2, Appl
19	2173	86.4	451	4	US-09-680-145-2 Sequence 2, Appl
20	2170	86.3	451	2	US-08-887-352B-14 Sequence 14, Appl
21	2170	86.3	451	3	US-08-887-352B-16 Sequence 16, Appl
22	2170	86.3	451	3	US-08-466-151-65 Sequence 65, Appl
23	2170	86.3	451	3	US-09-109-207C-14 Sequence 14, Appl
24	2170	86.3	451	3	US-09-109-207C-16 Sequence 16, Appl
25	2170	86.3	451	3	US-09-296-005-14 Sequence 14, Appl
26	2170	86.3	451	3	US-09-296-005-16 Sequence 16, Appl
27	2117	84.2	476	2	US-08-378-939-10 Sequence 10, Appl

28	2113	84.0	443	5	PCT-US96-13152-4	Sequence 4, Appl
29	2104.5	83.7	467	1	US-08-704-744-81	Sequence 81, Appl
30	2100.5	83.6	468	4	US-09-485-737B-67	Sequence 67, Appl
31	2100.5	83.6	711	4	US-09-485-737B-90	Sequence 90, Appl
32	2094.5	83.3	467	3	US-09-049-672A-8	Sequence 8, Appl
33	2092	83.2	476	3	US-08-487-550-12	Sequence 12, Appl
34	2092	83.2	476	4	US-09-526-098-12	Sequence 12, Appl
35	2090.5	83.2	473	3	US-09-049-672A-4	Sequence 4, Appl
36	2089	83.1	446	1	US-08-458-516-13	Sequence 13, Appl
37	2086.5	83.0	449	3	US-08-397-411-7	Sequence 7, Appl
38	2062	82.0	472	4	US-08-793-450-8	Sequence 8, Appl
39	2062	82.0	472	4	US-09-301-593-43	Sequence 43, Appl
40	2060	81.9	472	4	US-09-301-593-30	Sequence 30, Appl
41	2046	81.4	476	3	US-08-487-550-4	Sequence 4, Appl
42	2046	81.4	476	4	US-09-526-098-4	Sequence 4, Appl
43	2044.5	81.3	453	4	US-09-301-593-18	Sequence 18, Appl
44	2037	81.0	451	4	US-09-247-352-3	Sequence 3, Appl
45	2037	81.0	451	4	US-09-466-635-3	Sequence 3, Appl

## ALIGNMENTS

RESULT 1  
US-08-157-101A-7  
Sequence 7, Application US/08157101A  
Patent No. 5808032  
GENERAL INFORMATION:  
APPLICANT: KURIHARA, TATSUYA  
APPLICANT: MATSUKURA, SHIGEKAZU  
APPLICANT: TSURUOKA, NOBUO  
APPLICANT: ARIMA, KENJI  
APPLICANT: NISHIHARA, TATSURO  
TITLE OF INVENTION: ANTI-HBS ANTIBODY GENES AND EXPRESSION  
TITLE OF INVENTION: PLASMIDS THEREFOR  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PILLSBURY, MADISON & SUTRO  
STREET: 1100 NEW YORK AVENUE, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/157,101A  
FILING DATE: 05-APR-1994  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: TITUS, MARILAN K  
REGISTRATION NUMBER: 35843  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-861-3711  
TELEFAX: 202-822-0944  
TELEX: 671462Z CUCH  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 459 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-157-101A-7  
Query Match 88.4%; Score 2221.5; DB 1; Length 459;  
Best Local Similarity 89.9%; Pred. No. 2,1e-172;  
Matches 417; Conservative 19; Mismatches 23; Indels 5; Gaps 1;

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QY 11 VALIKGYOCEVLELSEGGGLVOPGSLRLSCAASGFTFSNYSAMSWROAPGKLEWVSAT 70
   1 VGLLRGVOQVQLVESGGGVQPGPSRLRLSCAASGFTFSNYSAMSWROAPGKLEWVAVI 60
QY 71 SASGHSYVLADSVKGRFTISRDNSKNTLYIQMNSLRADDAVYYCAKDREVTMTIVLNGG 130
   61 LYDENHNFYADSVKGRFTISRDNKNTLYIEVKSLQIEDTGVYCIIRDQDTGV-----HR 115
QY 131 FDYWGQGLTVVSSASTKGPVFLPAPSSKSTSGTALAGCLVADYFPEPTVSMNSGAL 190
   116 FDSWGQGLTVVSSASTKGPVFLPAPSSKSTSGTALAGCLVADYFPEPTVSMNSGAL 175
QY 191 TSVGHTPEPVALQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKPSNTKYDKKVEPKSCDKT 250
   176 ASGVHTPEPVALQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKPSNTKYDKKVEPKSCDKT 235
QY 251 HTCPPCAPAPLGGPSVFLPPPKPKDTLMSRTPRYTCVVVDVSHEDPEVKFNNYVDSGE 310
   236 HTCPPCAPAPLGGPSVFLPPPKPKDTLMSRTPRYTCVVVDVSHEDPEVKFNNYVDSGE 295
QY 311 VHNKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP 370
   296 VHNKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP 355
QY 371 REPOVYTLPPSRREMTKNQVSLTCLVKGFPYSDIAVEMESNGOPENNYKTTTPYLDSDGS 430
   356 REPOVYTLPPSRREMTKNQVSLTCLVKGFPYSDIAVEMESNGOPENNYKTTTPYLDSDGS 415
QY 431 FFYLSKLTVDKSRMQGNVFCSSVMHEALNHNHYTKSLSPGK 474
   416 FFYLSKLTVDKSRMQGNVFCSSVMHEALNHNHYTKSLSPGK 459
Db

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## RESULT 2

```

US-09-027-449-71
: Sequence 71, Application US/09027449
: Patent No. 6025158
: GENERAL INFORMATION:
: APPLICANT: Gonzalez, Tania R.
: APPLICANT: Presta, Steven R.
: TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
: TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
: NUMBER OF SEQUENCES: 72
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 1 DNA Way
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: WinPatIn (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/027,449
: FILING DATE: 20-Feb-1998
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 60/074,330
: FILING DATE: 22-Jan-1998
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 60/038,664
: FILING DATE: 21-Feb-1997
: ATTORNEY/AGENT INFORMATION:
: NAME: Love, Richard B.
: REGISTRATION NUMBER: 34,659
: REFERENCE/DOCKET NUMBER: PI085R3-2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 650/225-5530
: TELEFAX: 650/952-9881

```

```

: INFORMATION FOR SEQ ID NO: 71:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 452 amino acids
: TYPE: Amino Acid
: TOPOLOGY: Linear
: US-09-027-449-71

```

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Query Match      87.3%; Score 2193.5; DB 3; Length 452;
Best Local Similarity 91.2%; Pred. No. 3.8e-170;
Matches 417; Conservative 9; Mismatches 24; Indels 7; Gaps 2;

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QY 20 EVQLLEGGGGLVQPGGSLRLSCAASGFTFSNYSAMSWROAPGKLEWVSATISASGHSYTL 79
   1 EVQLVQSGGGLVQPGGSLRLSCAASGFTFSNYSAMSWROAPGKLEWVSATISASGHSYTL 60
QY 80 ADSVKGRTISRDNKNTLYIQMNSLRADDAVYYCAKDREVTMTIVLNGG- FDYWGQ 137
   61 NQKFGRTISRDNKNTLYIQMNSLRADDAVYYCAKDREVTMTIVLNGG- FDYWGQ 115
QY 138 TRVTYVSSASTKGPVFLPAPSSKSTSGTALAGCLVADYFPEPTVSMNSGALTSGYHTF 197
   116 TLVTYVSSASTKGPVFLPAPSSKSTSGTALAGCLVADYFPEPTVSMNSGALTSGYHTF 175
QY 198 PAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKPSNTKYDKKVEPKSCDKTHTCP 257
   176 PAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKPSNTKYDKKVEPKSCDKTHTCP 235
QY 258 APPELLGGPSVFLPPPKPKDTLMSRTPRYTCVVVDVSHEDPEVKFNNYVDSGEVHNKTK 317
   236 APPELLGGPSVFLPPPKPKDTLMSRTPRYTCVVVDVSHEDPEVKFNNYVDSGEVHNKTK 295
QY 318 PREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGPREPOVYT 377
   296 PREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGPREPOVYT 355
QY 378 LPSPREMTKNQVSLTCLVKGFPYSDIAVEMESNGOPENNYKTTTPYLDSDGSFFLYSKL 437
   356 LPSPREMTKNQVSLTCLVKGFPYSDIAVEMESNGOPENNYKTTTPYLDSDGSFFLYSKL 415
QY 438 TVDKSRMQGNVFCSSVMHEALNHNHYTKSLSPGK 474
   416 TVDKSRMQGNVFCSSVMHEALNHNHYTKSLSPGK 452
Db

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## RESULT 3

```

US-09-026-985-71
: Sequence 71, Application US/09026985
: Patent No. 613426
: GENERAL INFORMATION:
: APPLICANT: Gonzalez, Tania R.
: APPLICANT: Presta, Steven R.
: TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
: TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
: NUMBER OF SEQUENCES: 72
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 1 DNA Way
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: WinPatIn (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/026,985
: FILING DATE: 20-Feb-1998
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Love, Richard B.

```

```

;
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1085R3-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 452 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-026-985-71

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Query Match      87.3%; Score 2193.5; DB 3; Length 452;
Best Local Similarity 91.2%; Pred. No. 3.8e-170;
Matches 417; Conservative 9; Mismatches 24; Indels 7; Gaps 2;

```

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QY 20 EVQLLESGGGLVQPGSLRLSCAASGFTFSNTAMSVKROAPGKGLEWVAISAGHSTYL 79
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 EVQLVQSGGGLVQPGSLRLSCAASGYSFSSHYMHVVRQAPGKGLEWGYIDPSNGETTY 60
QY 80 ADVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKDRVETMIVLVNGG--FDYWGOG 137
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 NQKFGRTLSRDNSKNTAYLQMNSLRAEDTAVYYCARGD----YRYNGDMFEFDYWGOG 115
QY 138 TRFTVSSASTKGSPVFPLAPSSKSTSGCTAAAGCLVKDYFPEPVYVSNMNGALTSVHTF 197
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 116 TLVTYSSASTKGSPVFPLAPSSKSTSGCTAAAGCLVKDYFPEPVYVSNMNGALTSVHTF 175
QY 198 PAVLQSSGLYSLSVVTVPSSSLGTQTYICNVNHRKPSNTRVDKRVKPSGCDKTHTCPPCP 257
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 176 PAVLQSSGLYSLSVVTVPSSSLGTQTYICNVNHRKPSNTRVDKRVKPSGCDKTHTCPPCP 235
QY 258 APELLGGPSVFLFPPPKKDTLMISRTPEVTCVVDVSHEDPEVKFMYVDGVEVHNAKTR 317
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 236 APELLGGPSVFLFPPPKKDTLMISRTPEVTCVVDVSHEDPEVKFMYVDGVEVHNAKTR 295
QY 318 PREEOYNSTYRVVSVLTVLDHOMLNGEKYCKVSNKALPAPIEKTSKAKGQPREPQVY 377
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 296 PREEOYNSTYRVVSVLTVLDHOMLNGEKYCKVSNKALPAPIEKTSKAKGQPREPQVY 355
QY 378 LPPSRDEMTKNQVSLTCLVKGFYPSDIAVWESNCGPENNYKTTTPVLDSDGSFFLYSKL 437
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 356 LPPSRDEMTKNQVSLTCLVKGFYPSDIAVWESNCGPENNYKTTTPVLDSDGSFFLYSKL 415
QY 438 TVDKSRMOQGNVFCSCVMHEALHNHYTQKSLSLSPGK 474
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 416 TVDKSRMOQGNVFCSCVMHEALHNHYTQKSLSLSPGK 452

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## RESULT 4

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US-09-121-952A-71
; Sequence 71, Application US/09121952A
; Patent No. 6458355
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc., Hsiei, Vanessa
; APPLICANT: Koumenis, Iphigenia
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Shahrokh, Zahra
; APPLICANT: Zapata, Gerardo A.
; TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

```

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk
; COMPUTER: IBM PC compatible

```

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;
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09121,952A
; FILING DATE: 24-JUL-1998
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/074330
; FILING DATE: 22-JAN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/075467
; FILING DATE: 20-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1085R4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 452 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-121-952A-71

```

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Query Match      87.3%; Score 2193.5; DB 4; Length 452;
Best Local Similarity 91.2%; Pred. No. 3.8e-170;
Matches 417; Conservative 9; Mismatches 24; Indels 7; Gaps 2;

```

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QY 20 EVQLLESGGGLVQPGSLRLSCAASGFTFSNTAMSVKROAPGKGLEWVAISAGHSTYL 79
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 EVQLVQSGGGLVQPGSLRLSCAASGYSFSSHYMHVVRQAPGKGLEWGYIDPSNGETTY 60
QY 80 ADVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKDRVETMIVLVNGG--FDYWGOG 137
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 NQKFGRTLSRDNSKNTAYLQMNSLRAEDTAVYYCARGD----YRYNGDMFEFDYWGOG 115
QY 138 TRFTVSSASTKGSPVFPLAPSSKSTSGCTAAAGCLVKDYFPEPVYVSNMNGALTSVHTF 197
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 116 TLVTYSSASTKGSPVFPLAPSSKSTSGCTAAAGCLVKDYFPEPVYVSNMNGALTSVHTF 175
QY 198 PAVLQSSGLYSLSVVTVPSSSLGTQTYICNVNHRKPSNTRVDKRVKPSGCDKTHTCPPCP 257
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 176 PAVLQSSGLYSLSVVTVPSSSLGTQTYICNVNHRKPSNTRVDKRVKPSGCDKTHTCPPCP 235
QY 258 APELLGGPSVFLFPPPKKDTLMISRTPEVTCVVDVSHEDPEVKFMYVDGVEVHNAKTR 317
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 236 APELLGGPSVFLFPPPKKDTLMISRTPEVTCVVDVSHEDPEVKFMYVDGVEVHNAKTR 295
QY 318 PREEOYNSTYRVVSVLTVLDHOMLNGEKYCKVSNKALPAPIEKTSKAKGQPREPQVY 377
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 296 PREEOYNSTYRVVSVLTVLDHOMLNGEKYCKVSNKALPAPIEKTSKAKGQPREPQVY 355
QY 378 LPPSRDEMTKNQVSLTCLVKGFYPSDIAVWESNCGPENNYKTTTPVLDSDGSFFLYSKL 437
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 356 LPPSRDEMTKNQVSLTCLVKGFYPSDIAVWESNCGPENNYKTTTPVLDSDGSFFLYSKL 415
QY 438 TVDKSRMOQGNVFCSCVMHEALHNHYTQKSLSLSPGK 474
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 416 TVDKSRMOQGNVFCSCVMHEALHNHYTQKSLSLSPGK 452

```

## RESULT 5

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US-09-234-340A-71
; Sequence 71, Application US/09234340A
; Patent No. 6468532
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc., Hsiei, Vanessa
; APPLICANT: Koumenis, Iphigenia
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Shahrokh, Zahra

```



Db	6	GGGEWVGFIRNKPNGTTEVLAASVKDRFTTISRDDSKSLAIQLQMSLSLKIEDPAVYCT--	119
QY	119	REYTMIVLNG-----FDYWGQTRVTVSSASTKGPVSVP LAPSSKSTSGGTAALGCL	172
Db	119	--TSYISHCRGGVCGYGFEEFWGGQALTVSSASTKGPVSVP LAPSSKSTSGGTAALGCL	176
QY	173	VNDYPEPPTVSMNSGALITSGVHTFPAYLQSSGLYSLSSVYITVPSSSLGQTYYICNVNHK	232
Db	177	VNDYPEPPTVSMNSGALITSGVHTFPAYLQSSGLYSLSSVYITVPSSSLGQTYYICNVNHK	236
QY	233	PSNTKKDKRVEKSCDKTHTCCPPCAPRLGLGSPVFLPPIPRKDTLMISTRPEVTCVVD	292
Db	237	PSNTKKDKRVEKSCDKTHTCCPPCAPRLGLGSPVFLPPIPRKDTLMISTRPEVTCVVD	296
QY	293	VSHDEPEVKFNMYVDGVEVHNATKPRBEQYNSTYRVVSYITVLHQLMNGKEVCKVSN	352
Db	297	VSHDEPEVKFNMYVDGVEVHNATKPRBEQYNSTYRVVSYITVLHQLMNGKEVCKVSN	356
QY	353	KALPAIEKTIKAGQPREPOVYTLPPSRREDMTKNQVSLICLVKGGYPSDIAVEMESNG	412
Db	357	KALPAIEKTIKAGQPREPOVYTLPPSRDELTKNOVSLICLVKGGYPSDIAVEMESNG	416
QY	413	OPENNYKTPPVLDSGSPFLSKLTJVDSKRMQGNVFCSVMEALAHNHYTKSLSLSP	472
Db	417	OPENNYKTPPVLDSGSPFLSKLTJVDSKRMQGNVFCSVMEALAHNHYTKSLSLSP	476
QY	473	GK 474	
Db	477	GK 478	
RESULT 8			
US-09-679-397-2			
: Sequence 2, Application US/09679397			
: Patent No. 6339142			
: GENERAL INFORMATION:			
: APPLICANT: BASEY, CAROL D.			
: APPLICANT: BLANK, GREG S.			
: TITLE OF INVENTION: PROTEIN PURIFICATION			
: FILE REFERENCE: P1241RID2			
: CURRENT APPLICATION NUMBER: US/09/679,397			
: PRIOR FILING DATE: 2000-10-03			
: PRIOR APPLICATION NUMBER: US 60/084,459			
: PRIOR FILING DATE: 1998-05-06			
: PRIOR APPLICATION NUMBER: US 09/304,465			
: PRIOR FILING DATE: 1999-05-03			
: NUMBER OF SEQ ID NOS: 2			
: SEQ ID NO 2			
: LENGTH: 449			
: TYPE: PRT			
: ORGANISM: Artificial sequence			
: FEATURE:			
: OTHER INFORMATION: Sequence is synthesized.			
US-09-679-397-2			
Query Match			
Best Local Similarity 86.8%; Score 2181.5; DB 4; Length 449;			
Matches 416; Conservative 8; Mismatches 20; Indels 15; Gaps 2			
QY	20	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNYAMSWRQIPGKLEWVSAISAGHSTYL	79
Db	1	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNYAMSWRQIPGKLEWVSAISAGHSTYL	60
QY	80	ADSVKGRFTISRDNSKNTLYIOMNSLRADIEDPAVYYCAKDIEVTMIVLNG-----FDYW	134
Db	61	ADSVKGRFTISRDNSKNTLYIOMNSLRADIEDPAVYYCSR-----WGDDGFAMDTW	110
QY	135	GGSTRVTVSSASTKGPVSFPLAPSSKSTSGGTAALGCLVTDYPEPPTVSMNSGALITSGV	194
Db	111	GGGLTVTVSSASTKGPVSFPLAPSSKSTSGGTAALGCLVTDYPEPPTVSMNSGALITSGV	170
QY	195	HFPFPAVLOSSGLYSLSSVYTPSSSLGQTYYICNVNHKPRKDKRVEKSCDKTHTCC	254

```
Db 171 HTPFAVLQSSGLVSLSSVTVTPSSSLGTQYICNVNHRPSNTKVKDKVEPKSCDKTHTCP 230
Qy 255 PCPAPELLGGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNNWYVDGEVHNA 314
Db 231 PCPAPELLGGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNNWYVDGEVHNA 290
Qy 315 KTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ 374
Db 291 KTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ 350
Qy 375 VYTIAPSRREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNNKTPPVLDSDGSFFLY 434
Db 351 VYTIAPSRREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNNKTPPVLDSDGSFFLY 410
Qy 435 SKLTVDKSRMQQGNVFCSCVMHEALHNHYTQKSLSLSPG 473
Db 411 SKLTVDKSRMQQGNVFCSCVMHEALHNHYTQKSLSLSPG 449

RESULT 9
US-09-680-148-2
; Sequence 2, Application US/09680148
; Patent No. 6417335
; GENERAL INFORMATION:
; APPLICANT: BASEY, CAROL D.
; APPLICANT: BLANK, GREG S.
; TITLE OF INVENTION: PROTEIN PURIFICATION
; FILE REFERENCE: P1241R101
; CURRENT APPLICATION NUMBER: US/09/680,148
; CURRENT FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: US 60/084,459
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: US 09/304,465
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 2
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized.
; Patent No. 6417335
US-09-680-148-2

Query Match 86.8%; Score 2181.5; DB 4; Length 449;
Best Local Similarity 90.6%; Pred. No. 3,5e-169;
Matches 416; Conservative 8; Mismatches 20; Indels 15; Gaps 2;

Qy 20 EVQLLEGGGGLVPGGSLRLSCAASGFTFSNYAMSWVRQAPGKLEWVSATISAGHSTYL 79
Db 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSNYAMSWVRQAPGKLEWVSATISAGHSTYL 60
Qy 80 ADSVKGRFTTISADSKNTATLQMNSLRAEDTAVYVYCAKDRVTMIVLNGG-----FDYW 134
Db 61 ADSVKGRFTTISADSKNTATLQMNSLRAEDTAVYVYCAKDRVTMIVLNGG-----FDYW 110
Qy 135 GGGTRVTVSSASTGSPVFLPAPSSKSTSGGTALGCLVYKDPPEPYTVSNNGALTSV 194
Db 111 GGGTRVTVSSASTGSPVFLPAPSSKSTSGGTALGCLVYKDPPEPYTVSNNGALTSV 170
Qy 195 HTPFAVLQSSGLVSLSSVTVTPSSSLGTQYICNVNHRPSNTKVKDKVEPKSCDKTHTCP 254
Db 171 HTPFAVLQSSGLVSLSSVTVTPSSSLGTQYICNVNHRPSNTKVKDKVEPKSCDKTHTCP 230
Qy 255 PCPAPELLGGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNNWYVDGEVHNA 314
Db 231 PCPAPELLGGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNNWYVDGEVHNA 290
Qy 315 KTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ 374
Db 291 KTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ 350
Qy 375 VYTIAPSRREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNNKTPPVLDSDGSFFLY 434
Db 351 VYTIAPSRREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNNKTPPVLDSDGSFFLY 410
```

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Db 351 VYTIAPSRREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNNKTPPVLDSDGSFFLY 410
Qy 435 SKLTVDKSRMQQGNVFCSCVMHEALHNHYTQKSLSLSPG 473
Db 411 SKLTVDKSRMQQGNVFCSCVMHEALHNHYTQKSLSLSPG 449

RESULT 10
US-09-304-465A-2
; Sequence 2, Application US/09304465A
; Patent No. 6489447
; GENERAL INFORMATION:
; APPLICANT: BASEY, CAROL D.
; APPLICANT: BLANK, GREG S.
; TITLE OF INVENTION: PROTEIN PURIFICATION
; FILE REFERENCE: P1241R1
; CURRENT APPLICATION NUMBER: US/09/304,465A
; CURRENT FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/084,459
; PRIOR FILING DATE: 1998-05-06
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 2
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized.
; Patent No. 6489447
US-09-304-465A-2

Query Match 86.8%; Score 2181.5; DB 4; Length 449;
Best Local Similarity 90.6%; Pred. No. 3,5e-169;
Matches 416; Conservative 8; Mismatches 20; Indels 15; Gaps 2;

Qy 20 EVQLLEGGGGLVPGGSLRLSCAASGFTFSNYAMSWVRQAPGKLEWVSATISAGHSTYL 79
Db 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSNYAMSWVRQAPGKLEWVSATISAGHSTYL 60
Qy 80 ADSVKGRFTTISADSKNTATLQMNSLRAEDTAVYVYCAKDRVTMIVLNGG-----FDYW 134
Db 61 ADSVKGRFTTISADSKNTATLQMNSLRAEDTAVYVYCAKDRVTMIVLNGG-----FDYW 110
Qy 135 GGGTRVTVSSASTGSPVFLPAPSSKSTSGGTALGCLVYKDPPEPYTVSNNGALTSV 194
Db 111 GGGTRVTVSSASTGSPVFLPAPSSKSTSGGTALGCLVYKDPPEPYTVSNNGALTSV 170
Qy 195 HTPFAVLQSSGLVSLSSVTVTPSSSLGTQYICNVNHRPSNTKVKDKVEPKSCDKTHTCP 254
Db 171 HTPFAVLQSSGLVSLSSVTVTPSSSLGTQYICNVNHRPSNTKVKDKVEPKSCDKTHTCP 230
Qy 255 PCPAPELLGGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNNWYVDGEVHNA 314
Db 231 PCPAPELLGGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNNWYVDGEVHNA 290
Qy 315 KTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ 374
Db 291 KTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ 350
Qy 375 VYTIAPSRREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNNKTPPVLDSDGSFFLY 434
Db 351 VYTIAPSRREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNNKTPPVLDSDGSFFLY 410
Qy 435 SKLTVDKSRMQQGNVFCSCVMHEALHNHYTQKSLSLSPG 473
Db 411 SKLTVDKSRMQQGNVFCSCVMHEALHNHYTQKSLSLSPG 449

RESULT 11
US-08-466-151-8
; Sequence 8, Application US/08466151
; Patent No. 6037453
; GENERAL INFORMATION:
```



Db 416 LTVDKSRWQGNVFCSCVMHEALHNHYTKSLSPGK 453

## RESULT 13

US-08-887-352B-18

; Sequence 18, Application US/08887352B  
; Patent No. 5994511  
; GENERAL INFORMATION:  
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe  
; TITLE OF INVENTION: Improved Anti-1ge Antibodies and Method of  
; TITLE OF INVENTION: Improving Polypeptides  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Winpatin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/887,352B  
; FILING DATE: 03-Jul-1997  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Svoboda, Craig G.  
; REGISTRATION NUMBER: 39,044  
; REFERENCE/DOCKET NUMBER: P1123  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-1489  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 451 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-08-887-352B-18

Query Match 86.4%; Score 2173; DB 2; Length 451;

Best Local Similarity 90.8%; Pred. No. 1.7e-168;

Matches 414; Conservative 13; Mismatches 23; Indels 6; Gaps 3;

QY 20 EVOLLESGGLVOPGGSRLSCASGTF-SNYAMSWROAPRGLEWVASIASGSHSTY 78  
DB 1 EVOLVESGGGLVOPGGSRLSCASGYSITSGYSMMWIRAPRGLEWVASIKYSGETKY 60  
QY 79 LADSVKGRFTISRDNKNTLYLQNMNSLAEDTAVAYYCAKDREYTMIVVINGCFDYMGOGT 138  
DB 61 -NPSVKGRFTISRDNKNTLYLQNMNSLAEDTAVAYYCAKRGSH----YGHMHPFAMWOGGT 115  
QY 139 RVTVSSASTKGPVSFPLAPSSKSTSGTAAIGCLVKDYFPEPVTVSMNSGALTSGVHTFP 198  
DB 116 LVTVSSASTKGPVSFPLAPSSKSTSGTAAIGCLVKDYFPEPVTVSMNSGALTSGVHTFP 175  
QY 199 AVLOSGLYSLSSVTVVPSSTSLGTQTYICNVNHRPSNKKVDKKEPKSCDTHHCPCPPA 258  
DB 176 AVLOSGLYSLSSVTVVPSSTSLGTQTYICNVNHRPSNKKVDKKEPKSCDTHHCPCPPA 235  
QY 259 PELLGSPVFLFPPKPKDMLISRTPEYTCVVVDVSHEDPEVKFMWYDGEVHNAAKTKP 318  
DB 236 PELLGSPVFLFPPKPKDMLISRTPEYTCVVVDVSHEDPEVKFMWYDGEVHNAAKTKP 295  
QY 319 REEOYNSTYRVVSVLTVLHDWLNKGEYCKCKVSNKALPAPIEKTISKAKGQPREPOVYTL 378  
DB 296 REEOYNSTYRVVSVLTVLHDWLNKGEYCKCKVSNKALPAPIEKTISKAKGQPREPOVYTL 355  
QY 379 PPSREEMTKNOVSLTCLVKGFPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLT 438

Db 356 PPSREEMTKNOVSLTCLVKGFPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLT 415  
QY 439 VDKSRWQGNVFCSCVMHEALHNHYTKSLSPGK 474  
DB 416 VDKSRWQGNVFCSCVMHEALHNHYTKSLSPGK 451

## RESULT 14

US-09-109-207C-18

; Sequence 18, Application US/09109207C  
; Patent No. 6172213  
; GENERAL INFORMATION:  
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe  
; TITLE OF INVENTION: Improved Anti-1ge Antibodies and Method of Improving Polypept  
; FILE REFERENCE: P1123R1  
; CURRENT APPLICATION NUMBER: US/09/109,207C  
; PRIOR FILING DATE: 1998-06-30  
; PRIOR APPLICATION NUMBER: US 60/051,554  
; NUMBER OF SEQ ID NOS: 44  
; SEQ ID NO 18  
; LENGTH: 451  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; NAME/KEY: Artificial  
; LOCATION: 1-451  
; OTHER INFORMATION: Heavy chain sequence derived from MAE11  
US-09-109-207C-18

Query Match 86.4%; Score 2173; DB 3; Length 451;

Best Local Similarity 90.8%; Pred. No. 1.7e-168;

Matches 414; Conservative 13; Mismatches 23; Indels 6; Gaps 3;

QY 20 EVOLLESGGLVOPGGSRLSCASGTF-SNYAMSWROAPRGLEWVASIASGSHSTY 78  
DB 1 EVOLVESGGGLVOPGGSRLSCASGYSITSGYSMMWIRAPRGLEWVASIKYSGETKY 60  
QY 79 LADSVKGRFTISRDNKNTLYLQNMNSLAEDTAVAYYCAKDREYTMIVVINGCFDYMGOGT 138  
DB 61 -NPSVKGRFTISRDNKNTLYLQNMNSLAEDTAVAYYCAKRGSH----YGHMHPFAMWOGGT 115  
QY 139 RVTVSSASTKGPVSFPLAPSSKSTSGTAAIGCLVKDYFPEPVTVSMNSGALTSGVHTFP 198  
DB 116 LVTVSSASTKGPVSFPLAPSSKSTSGTAAIGCLVKDYFPEPVTVSMNSGALTSGVHTFP 175  
QY 199 AVLOSGLYSLSSVTVVPSSTSLGTQTYICNVNHRPSNKKVDKKEPKSCDTHHCPCPPA 258  
DB 176 AVLOSGLYSLSSVTVVPSSTSLGTQTYICNVNHRPSNKKVDKKEPKSCDTHHCPCPPA 235  
QY 259 PELLGSPVFLFPPKPKDMLISRTPEYTCVVVDVSHEDPEVKFMWYDGEVHNAAKTKP 318  
DB 236 PELLGSPVFLFPPKPKDMLISRTPEYTCVVVDVSHEDPEVKFMWYDGEVHNAAKTKP 295  
QY 319 REEOYNSTYRVVSVLTVLHDWLNKGEYCKCKVSNKALPAPIEKTISKAKGQPREPOVYTL 378  
DB 296 REEOYNSTYRVVSVLTVLHDWLNKGEYCKCKVSNKALPAPIEKTISKAKGQPREPOVYTL 355  
QY 379 PPSREEMTKNOVSLTCLVKGFPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLT 438  
DB 356 PPSREEMTKNOVSLTCLVKGFPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLT 415  
QY 439 VDKSRWQGNVFCSCVMHEALHNHYTKSLSPGK 474  
DB 416 VDKSRWQGNVFCSCVMHEALHNHYTKSLSPGK 451

## RESULT 15

US-09-282-505-2

; Sequence 2, Application US/09282505A  
; Patent No. 6194551  
; GENERAL INFORMATION:  
; APPLICANT: Esche Eklinaduse Idusogie et al.



; TITLE OF INVENTION: Polypeptide Variants  
; FILE REFERENCE: P1266R1  
; CURRENT APPLICATION NUMBER: US/09/282,505A  
; CURRENT FILING DATE: 1999-03-31  
; NUMBER OF SEQ ID NOS: 2  
; SEQ ID NO 2  
; LENGTH: 451  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: Artificial Sequence  
; LOCATION: 1-451  
; OTHER INFORMATION: Sequence is completely synthesized  
; Patent No. 6194551  
US-09-282-505-2

Query Match 86.4%; Score 2173; DB 3; Length 451;  
Best Local Similarity 90.8%; Pred. No. 1.7e-168;  
Matches 414; Conservative 13; Mismatches 23; Indels 6; Gaps 3;

OY 20 EVOLLEGGGLVOPGSLRLSCAAGTF-SNYAMSWYRQAPGKLEWYSAISAGHSTY 78  
DB 1 EVQLVESGGGLVQPGSLRLSCAASGYSITSGYSWMWIRQAPGKLEWVASIKYSGETKY 60  
OY 79 LADSVKGRFTISRDNKNTLYIQMNSLRAPDPAVYYCAKDRVETMIIVLNGGFDYWGOTT 138  
DB 61 -NPSTYKGRITISRDNKNTLYIQMNSLRAPDPAVYYCAKDRVETMIIVLNGGFDYWGOTT 115  
OY 139 RVTYSSASTKGPSPVFPLAPSSKSTSGTAALGCLVKDYFPEPVYVSWNSGALTSGVHTEP 198  
DB 116 LVTYSSASTKGPSPVFPLAPSSKSTSGTAALGCLVKDYFPEPVYVSWNSGALTSGVHTEP 175  
OY 199 AVLOSGLYSLSVYTVPSSSSLGTOTYICNNVHKSNTKVDKRVPEKSCDKTHTCPCPA 258  
DB 176 AVLOSGLYSLSVYTVPSSSSLGTOTYICNNVHKSNTKVDKRVPEKSCDKTHTCPCPA 235  
OY 259 PELGGSPVFLEPPPKDITLMSRPEVTCVYVDVSHEDPEYKFNMYVDGVEVHNAKTRP 318  
DB 236 PELGGSPVFLEPPPKDITLMSRPEVTCVYVDVSHEDPEYKFNMYVDGVEVHNAKTRP 295  
OY 319 REEOYNSTYRVSVLTVLHODMLNGEKYCKVSNKALPAPIEKTIISKAKGQPREPOVYTL 378  
DB 296 REEOYNSTYRVSVLTVLHODMLNGEKYCKVSNKALPAPIEKTIISKAKGQPREPOVYTL 355  
OY 379 PPSREEMTKNOVSLTCLVKGFPYSDIAVEWESNGOPENNYKTPPYLDSDGSFFLYSKLT 438  
DB 356 PPSREEMTKNOVSLTCLVKGFPYSDIAVEWESNGOPENNYKTPPYLDSDGSFFLYSKLT 415  
OY 439 VDKSRMOQGNVFCSCVMHEALHNHYTOKSLSPGK 474  
DB 416 VDKSRMOQGNVFCSCVMHEALHNHYTOKSLSPGK 451

Search completed: September 12, 2003, 13:05:13  
Job time : 28.7797 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 12, 2003, 12:56:44 : Search time 82.3475 Seconds  
(without alignments)  
1485.376 Million cell updates/sec

Title: US-09-848-832-3

Perfect score: 2514  
Sequence: 1 MEFGLSMFLFVAILKGYCE.....MHEALHNHTOKSLSPCK 474

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues  
Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL.23:\*  
1: sp.archaea:\*  
2: sp.bacteria:\*  
3: sp.fungi:\*  
4: sp.human:\*  
5: sp.invertebrate:\*  
6: sp.mammal:\*  
7: sp.mhc:\*  
8: sp.organelle:\*  
9: sp.phage:\*  
10: sp.plant:\*  
11: sp.rodent:\*  
12: sp.virus:\*  
13: sp.vertibrate:\*  
14: sp.unclassified:\*  
15: sp.rvirus:\*  
16: sp.bacteriap:\*  
17: sp.archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2325.5	92.5	471	4	Q8TC77 homo sapien
2	2105.5	83.8	521	4	Q8N4Y9 homo sapien
3	1882	74.9	473	4	Q8TC63 homo sapien
4	1660.5	66.1	469	11	Q8R3V9 mus musculu
5	1625.5	64.7	509	4	Q8NFI7 homo sapien
6	1587.5	63.1	473	11	Q91Z05 mus musculu
7	1541.5	60.1	437	11	Q9R1A4 mus musculu
8	1511.5	59.5	463	11	Q9R1C4 mus musculu
9	1495.5	58.6	468	11	Q9R1C4 mus musculu
10	1474	57.5	473	11	Q9R1C4 mus musculu
11	1446.5	56.2	473	11	Q9R1C4 mus musculu
12	1414	55.0	474	11	Q9R1C4 mus musculu
13	1263.5	50.3	337	6	Q95M34 equus cabal
14	1257	50.0	701	4	Q96F08 homo sapien
15	1061.5	42.2	597	4	Q96B89 homo sapien
16	1010	40.2	613	4	Q8WTK1 homo sapien

17	929	37.0	494	4	Q96K68 homo sapien
18	926.5	36.9	499	4	Q8N5K4 homo sapien
19	907.5	36.1	493	4	Q8NCL6 homo sapien
20	897.5	35.7	467	11	Q99KA4 mus musculu
21	866.5	34.5	479	11	Q91WP5 mus musculu
22	846	33.7	486	11	Q91Z07 mus musculu
23	822.5	32.7	480	11	Q91XE1 mus musculu
24	811	32.3	484	11	Q8VEA0 mus musculu
25	775	30.8	573	4	Q8WU38 homo sapien
26	757	30.1	613	11	Q8VCX7 mus musculu
27	755.5	30.1	597	4	Q9BU10 homo sapien
28	755	30.0	278	11	Q921K1 mus musculu
29	754.5	30.0	614	4	Q96GA5 mus musculu
30	753.5	30.0	597	4	Q9BDB8 homo sapien
31	746	29.7	513	4	Q96EY0 homo sapien
32	745.5	29.7	588	4	Q8WUX4 homo sapien
33	745.5	29.7	618	4	Q96AA6 homo sapien
34	724	28.8	500	4	Q9BRV0 homo sapien
35	702.5	27.9	497	4	Q8WY24 homo sapien
36	701	27.9	484	11	Q991A6 mus musculu
37	697.5	27.7	481	11	Q91WT1 mus musculu
38	692	27.5	482	11	Q91X92 mus musculu
39	692	27.5	496	4	Q96DK0 homo sapien
40	691	27.5	482	11	Q8K172 mus musculu
41	687	27.3	480	11	Q8K0Z4 mus musculu
42	681	27.1	486	4	Q96KX8 homo sapien
43	678	26.8	488	11	Q8K0F2 mus musculu
44	673.5	26.8	489	11	Q8VCX4 mus musculu
45	670	26.7	488	11	Q91WR1 mus musculu

## ALIGNMENTS

## RESULT 1

Q8TC77 PRELIMINARY: PRT; 471 AA.  
ID Q8TC77;  
AC Q8TC77;  
DT 01-JUN-2002 (TREMBLrel. 21, Created)  
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update\*)  
DE Hypothetical protein.  
OS Homo sapiens (human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAUSBERG R.;  
RA Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
RL EMBL; BC024289; AAH24289.1;  
DR InterPro: IPR007110; Ig\_Like.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003596; Ig\_V.  
DR Pfam: PF00047; Ig; 4.  
DR SMART: SM00406; IgV; 1.  
DR PROSITE: PS50835; IG\_LIKE; 4.  
DR PROSITE: PS00290; IG\_MHC; 2.  
KW Hypothetical protein  
SQ SEQUENCE 471 AA; 51791 MW; 3887F4CF58660E C'RC64;

Query Match 92.5%; Score 2325.5; DB 4; Length 471;  
Best Local Similarity 92.2%; Pred. No. 2.2e-183;  
Matches 438; Conservative 19; Mismatches 13; Indels 5; Gaps 2;

Qy	1	MEFGLSMFLFVAILKGYCEVQLLESGGIVGCGSIRLS;AASGFTFSYANASWYRQAP 60
Db	1	MEGLSMFLFVAILKEGYCEVQLLESGGIVGCGSIRLS;AASGFTFSYANASWYRQAP 60
Qy	61	GKLEWVASASGSHSTYADSVKGRFTISRDNKNTLY;JMSLAEDPAVYCKAD-R 119
Db	61	GKLEWVASASGSHSTYADSVKGRFTISRDNKNTLY;JMSLAEDPAVYCKAD-R 120

QY	120	VVTMLVLVUNGCGDYACGGRVYVASTGCVSVFLPAPBSKSTSGGTAALGCLVKQDPE	179
Dd	121	QILSTWY----FDLNGKGLTVYVSSAKTGPSPFPLAPBSKSTSGGTAALGCLVKQYFPE	176
QY	180	PVTWSMNGALITSGVHTFPPAVLQSSGGLSLSSVVTIPSSSLGTQTYICVNHKPSMTKYD	239
Dd	177	PVTWSMNGALITSGVHTFPPAVLQSSGGLSLSSVVTIPSSSLGTQTYICVNHKPSMTKYD	236
QY	240	KRVKPSGDKTHTCPCPCAPPELLGGPSVFLFPPKPKDTLMISSTPEVTCVVDVSHEDPE	299
Dd	237	KKVEKSCDKHTKCPCCAPPELLGGPSVFLFPPKPKDTLMISSTPEVTCVVDVSHEDPE	296
QY	300	VKFNMYVDGVEVHNATKTPREEQYNSTYRVASVLTVLHODWLNKGEYKCKVSKNALPAPI	359
Dd	297	VKFNMYVDGVEVHNATKTPREEQYNSTYRVASVLTVLHODWLNKGEYKCKVSKNALPAPI	356
QY	360	EKTISKAKGQPEEPVYTLTPRSREMTKQVSLTCLVKKFYPSDIAVEMESNQPENNK	419
Dd	357	EKTISKAKGQPEEPVYTLTPRSREMTKQVSLTCLVKKFYPSDIAVEMESNQPENNK	416
QY	420	TTTPVLDSDGSFFLYSKLTVDKSRMQQGVFSCSVNHEALAHNYTOKSLSLSPGK	474
Dd	417	TTTPVLDSDGSFFLYSKLTVDKSRMQQGVFSCSVNHEALAHNYTOKSLSLSPGK	471

Query Match	83.8%	Score 2105.5	DB 4	Length 521
Best Local Similarity	77.2%	Pred. No. 3.6e-165		
Matches 404	Conservative 26	Mismatches 42	Indels 51	Gaps 3
QY	1	MEFLSLMFLVAIIKGVQCEVQLESGGGLVQPGSLRISCAASGFTFSNYMSVRQAP	60	
DB	1	MEFLSLMFLVAIIKGVQCEVQLESGGGLVQPGSLRISCAASGFTFSNYMSVRQAP	60	
QY	61	GKGEWWSAISASGH--STYLADSVKGRFTSRDMSKMTLYIOMNSLRADETAVYVCARD	118	
DB	61	GKGEWWSAISASGH--STYLADSVKGRFTSRDMSKMTLYIOMNSLRADETAVYVCARD	120	
QY	119	REVMIVVLUNGCPDYWGQGRVTVTSASTKGPSPYLAAPSRSKTSGGTAACTLVKDYPP	178	
DB	121	LEGA--GKYDMPDYIMWGRGLIVTVSSASTKGPSPYLAAPSRSKTSGGTAACTLVKDYPP	178	
QY	179	EPVTVSNNGALJISGVHTFPAVLQSSGLYSASSVTVPSSSLGTQTYICNVHKSPTKV	238	

Db	179	EPVYIWSANGALTSGVHTPPAYLQSSGLTSLSSVYTPVSSSLGTQTYTTCNVMHNPENTKY	238
QY	239	DKRV-----	EBKSCDKTH 251
Db	239	DKRVELKPTLGDYTHNCPRCPEPKSCDTPPCDPEPKSCDTPPCDPEPKSCDTPP	298
QY	232	TCPRCPEBLLAGSVEFLFRPKPKDTLMSIKRPEYTCVYVDVSHEDPEVKFNNYVDGVEY	311
Db	299	PCPRCPAEELLGGSVFLFRPKPKDTLMSIKRPEYTCVYVDVSHEDPEVKFNNYVDGVEY	358
QY	312	HNAAKPRPEEOYNSTYRYVSVLYTLHODMLNKEKCKCKYSNKALPAPIEKITSKAKGQPR	371
Db	359	HNAAKPRPEEOQNSTFRVYSVLYTLHODMLNKEKCKCKYSNKALPAPIEKITSKTKGQPR	418
QY	372	EPQVYTLPPSREEMTKNOVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTTPVYLDSDGEF	431
Db	419	EPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEMESGQPENNYNTTPMLDSDGSP	478
QY	432	FLYSKLTIVDKSRMOOGNVPSCGVMEHALHNHTQKSLSPGK	474
Db	479	FLYSKLTIVDKSRMOOGNIFSCGVMEHALHNRTQKSLSPGK	521

RESULT 3					
ID	Q8TC63	PRELIMINARY:	PRT:	473 AA.	
AC	Q8TC63;				
DT	01-JUN-2002 (TREMBLrel. 21, Created)				
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)				
DE	01-MAR-2003 (TREMBLrel. 23, Last annotation update)				
DE	Hypothetical protein.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_Taxid=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=kidney;				
RA	Strausberg R.;				
RL	Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.				
DR	EMBL: BC025985; AAA25985.1; -				
DR	InterPro: IPR000923; BlueCu_1.				
DR	InterPro: IPR007110; Ig-like.				
DR	InterPro: IPR003006; IG_MHC.				
DR	InterPro: IPR003596; Ig-v.				
DR	Pfam: PF00047; Ig_f. 4.				
DR	SMART: SMO0406; IGV: 1.				
DR	PROSITE: PS00196; COPPER_BLUE; 1.				
DR	PROSITE: PS50835; IG_LIKE; 4.				
DR	PROSITE: PS00290; IG_MHC; 3.				
KW	Hypothetical protein.				
SEQ	SEQUENCE 473 AA; 51986 MW; E29920B0D9A369F5 CRC64;				
	Query Match	74.9%;	Score 1882;	DB 4;	Length 473;
	Best Local Similarity	77.8%;	Pred. No. 8.7e-147;		
	Matches 368;	Conservative 31;	Mismatches 58;	Indels 16;	Gaps 6
QY	7 WLF--LVALLGVCCEVOLLSEGGGLVGPGSLRLSCAAAG--FFFSNYAMSWVRQAPEGK 62           :   :       :   :     :   :				
Dd	12 WFELLLVAAPRWVLSSLRLOLESPEPLKPVTLSLTCTVSIGGSVASSTSYMGWVROPPEK 71           A P R W V L S S L R L O L E S G P E L K P V T L S L T C T V S I G G S V A S S T Y M G W V R O P P E K				
QY	63 GLEVVSAISAGSHSTYLADSVKGRPTTISRNSKNITLYLOMNSLAEDTAIVYYCAKDREYT 122           :   :   :   :   :   :   :   :   :   :   :   :				
Dd	72 GLEMIGITINFG-KMYIYPSLRKYTKMAADSSENSFYKLDSVTATDAIVYYCAAGHLVM 130           I T N F G - K M Y I Y P S L R K Y T K M A D S E N S F Y K L D S V T A T D A I V Y Y C A A G H L V M				
QY	123 MIYVNGEFD-YWGOGTRVTYSASATKSPVFPIAPSSKSTSOGTALGLCKDYFPPEPV 181           :   :				
Dd	131 -----GFGAHMGQGKRILVSVSPAISTKGPSVFPLAPCSRSTSESRPALGLCKDYFPPEPV 183 				
QY	182 TVSNNGSALTSYGVTTPFAVLLOSSGLYLSSVYTVPPSSLGTOFTYCANNHKPNTKVDR 241           S A L T S Y G V T T P F A V L L O S S G L Y L S S V Y T V P P S S L G T O F T Y C A N N H K P N T K V D R				
Dd	184 TVSNNGSGALTSGVHTFPVALLOSSGLYLSSVYTVPPSSLSGTRKYTCNNVDHKPSNKKVKDR 243           S G A L T S G V H T F P V A L L O S S G L Y L S S V Y T V P P S S L S G T R K Y T C N N V D H K P S N K K V K D R				

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QY 242 VEPKSCDKTHCPAPAPELLGSPVFLFPPKPKDTLMISRTPEVTCVAVVDYSHDPEYK 301
DB 244 VESK---YGPCCPSCPAPPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVAVVDYSHDPEYK 300
QY 302 FNNYVDGVEVHNNAKTRPREEOYNSTYRVVSVLTIVHODMLNGKEVCKKSNKALPAPIEK 361
DB 301 FNNYVDGVEVHNNAKTRPREEOYNSTYRVVSVLTIVHODMLNGKEVCKKSNKALPAPIEK 360
QY 362 TISKAKGPREPOVYTLPPSREEMTKNOVSLTCLVKGFPYSDIAVEMESNGOPENNYKT 421
DB 361 TISKAKGPREPOVYTLPPSREEMTKNOVSLTCLVKGFPYSDIAVEMESNGOPENNYKT 420
QY 422 PPVLDSGSEFLYSKLTVDKSRMOQGNVFCSCVMHEALHNHTOKSLSPCK 474
DB 421 PPVLDSGSEFLYSKLTVDKSRMOQGNVFCSCVMHEALHNHTOKSLSPCK 473

RESULT 4
QY 08R3V9 PRELIMINARY: PRT: 469 AA.
AC 08R3V9;
DT 01-JUN-2002 (TREMblrel. 21, Created)
DT 01-JUN-2002 (TREMblrel. 21, last sequence update)
DE 01-MAR-2003 (TREMblrel. 23, last annotation update)
OS Hypothetical 52.0 kDa protein.
OC Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strusberg R.;
RL Submitted (MAR-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL: BC024405; AAH24405.1;
DR InterPro: IPR007110; Ig_Like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_4.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS00835; IG_LIKE; 4.
DR PROSITE: PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ
SEQUENCE 465 AA; 51976 MW; 534793F155D05457 CRC64;

Query Match 66.1%; Score 1660.5; DB 11; Length 469;
Best Local Similarity 64.2%; Pred. No. 1,6e-128;
Matches 307; Conservative 72; Mismatches 86; Indels 13; Gaps 6;

QY 1 MEFGLSWFLVAIILGVGCEVOLLESGGGLVOPGSGSLRLSCAASGFTFSNTYAMSWYKAP 60
DB 1 MFLWNLWIFLYTLNLGIDCEVNLVESGGGLVOPGSLRLSCAASGFTFDYVMSWYKAP 60
QY 61 GKGLMWSAI--SASGHSSTYLADSVKGRFTISRDNKNTLYLOMNSLRADPAVYVYCARD 118
DB 61 GKALMELGFTIRNKAKAGITTEYSASVAKGRFTISRDNKNTLYLOMNSLRADPAVYVYCARD 120
QY 119 REVVTIMVVLNGGFDYWGQGTTRVTVSSASTKGPVFPPLAPSSKSTSGGTALGLVNDYPP 178
DB 121 RR-SSYYYSCTSFAYWAGGTLVTYSAKTTTPSYVPLAPGSAAGTNSMTVTLGLVNGYPP 179
QY 179 EYVYVYVMSNGALITSGVHTFPYAVVQSSGLYSSVTVVPSLSLGTQTYICNVNHNKPSNTV 238
DB 180 EYVYVYVMSNGALITSGVHTFPYAVVQSSGLYSSVTVVPSLSLGTQTYICNVNHNKPSNTV 238
QY 239 DKRVKPSKCDKTHCP--CPAPELLGSPVFLFPPKPKDTLMISRTPEVTCVAVVDYSHD 296
DB 239 DKRIYPRDCG---CKPCLITVPEV---SSVFIIPPKPKDVLITITLTPKTCVAVVDISKD 291
QY 297 DPEVAFNNYVDGVEVHNNAKTRPREEOYNSTYRVVSVLTIVHODMLNGKEVCKKSNKALP 356
DB 292 DPEVQFSMFVDGVEVHTAQTFRPREQFNSTFRSVSELPIMHODMLNGKEVCKKSNKALP 351
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QY 357 APIEKTISKAKGPREPOVYTLPPSREEMTKNOVSLTCLVKGFPYSDIAVEMESNGOPEN 416
DB 352 APIEKTISKAKGPREPOVYTLPPSREEMTKNOVSLTCLVKGFPYSDIAVEMESNGOPEN 411
QY 417 NYKTPPPVLDSGSEFLYSKLTVDKSRMOQGNVFCSCVMHEALHNHTOKSLSPCK 474
DB 412 NYKTPPPVLDSGSEFLYSKLTVDKSRMOQGNVFCSCVMHEALHNHTOKSLSPCK 469

RESULT 5
QY 08NF17 PRELIMINARY: PRT: 509 AA.
ID 08NF17;
AC 08NF17;
DT 01-OCT-2002 (TREMblrel. 22, Created)
DT 01-OCT-2002 (TREMblrel. 23, last sequence update)
DE 01-MAR-2003 (TREMblrel. 23, last annotation update)
DE FLJ00385 protein (Fragment).
GN FLJ00385.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tissue-Spleen.
RA Jikuya H., Takano J., Kikuno R., Nagase T., Ohara O.;
RT "The nucleotide sequence of a long cDNA clone isolated from human spleen."
RL Submitted (JUL-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL: AK090464; BAC03445.1;
DR InterPro: IPR007110; Ig_Like.
DR InterPro: IPR003597; Ig_C1.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig1; 3.
DR SMART: SM00407; IGV; 1.
DR PROSITE: PS00835; IG_LIKE; 3.
DR PROSITE: PS00290; IG_MHC; 2.
FT NON_TER
SQ
SEQUENCE 509 AA; 56111 MW; 089498D8076E863C CRC64;

Query Match 64.7%; Score 1625.5; DB 4; Length 509;
Best Local Similarity 82.2%; Pred. No. 1,4e-125;
Matches 309; Conservative 9; Mismatches 11; Indels 47; Gaps 1;

QY 144 SASYKGPVFPPLAPSSKSTSGGTALGLVNDYFPPEVTVVWNSGALITSGVHTFPYAVLOS 203
DB 63 AASTKGPVFPPLAPSSKSTSGGTALGLVNDYFPPEVTVVWNSGALITSGVHTFPYAVLOS 122
QY 204 SGLYSLSSVTVVPSLSLGTQTYICNVNHNKPSNTKYDKRV----- 242
DB 123 SGLYSLSSVTVVPSLSLGTQTYICNVNHNKPSNTKYDKRV----- 242
QY 243 -----EPKSCDKTHCPAPAPELLGSPVFLFPPKPKD 276
DB 183 CDTPPCPKCPKSCDTPPPCPKCPKSCDTPPPCPKCPKSCDTPPPCPKCPKSCDTPPPCPK 242
QY 277 TLMISRTPEVTCVAVVDYSHDPEYKFNMYVDGVEVHNNAKTRPREEOYNSTYRVVSVLTIV 336
DB 243 TLMISRTPEVTCVAVVDYSHDPEYKFNMYVDGVEVHNNAKTRPREEOYNSTYRVVSVLTIV 302
QY 337 HODMLNGKEVCKKSNKALPAPIEKTISKAKGPREPOVYTLPPSREEMTKNOVSLTCLV 396
DB 303 HODMLNGKEVCKKSNKALPAPIEKTISKAKGPREPOVYTLPPSREEMTKNOVSLTCLV 362
QY 397 KGFYSDIAVEMESNGOPENNYKTTPPVLDSDSSEFLYSKLTVDKSRMOQGNVFCSCVMH 456
DB 363 KGFYSDIAVEMESNGOPENNYKTTPPVLDSDSSEFLYSKLTVDKSRMOQGNVFCSCVMH 422
QY 457 EALHNHTOKSLSP 472
DB 423 EALHNHTOKSLSP 438
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## RESULT 6

Q91205 PRELIMINARY; PRT; 473 AA.  
AC Q91205;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Hypothetical 51.9 kDa protein.  
GN AU044919.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Strausberg R.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC010327; AA010327.1; -  
DR MGI; MGI:2144967; AU044919.  
DR InterPro; IPR00345; CytC\_heme\_bind.  
DR InterPro; IPR007110; Ig\_Like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 3.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00190; CYTOCHROME\_C; 1.  
DR PROSITE; PS0835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 473 AA; 51946 MW; CF625F008932AF12 CRC64;

Query Match 63.1%; Score 1587.5; DB 11; Length 473;  
Best Local Similarity 62.6%; Pred. No. 1.7e-122;  
Matches 301; Conservative 70; Mismatches 95; Indels 15; Gaps 4;

QY 1 MEFLSNLEFLAIIKGVQCEVQLLESGGGLVQPGSGSLRSCAASGFTFSNAMSVMVRAP 60  
DB 1 MDSRLNLFVLLILKGVQCEVQLLESGGGLVQPGSGSLRSCAASGFTFSNAMSVMVRAP 60  
QY 61 GKGLEWVAISASGSHSTIADSVKGRFTISRDNKNTLYLQMSLRADETAVYCAKRE 120  
DB 61 EKGLEWVAISASGSHSTIADSVKGRFTISRDNKNTLYLQMSLRADETAVYCAKRE 120  
QY 121 VTMIIVNLNGFDYWGQGTIRTVVSASATKGPSVFPPLAPSSKSTSGTAAIGCLVNDYRPP 180  
DB 121 LRRF-----DYWGQGTIRTVVSASATKGPSVFPPLAPSSKSTSGTAAIGCLVNDYRPP 180  
QY 181 VTVMWNSGALTSVHTPRAVLQSSGLVSLSSVTVVPSSLSGTOTYICNVNHRKPSNTKYDK 240  
DB 174 VTVMWNSGALTSVHTPRALQ-SGLVTMSSSVTVPPSSVTPSQTVTCVAHPASSTTVDK 232  
QY 241 RVEPRSCDKT-HTCP-----CPAPELLGSPVFLFPKPKDTLMISRTPEVTCVYVDY 293  
DB 233 KLEISGSPSTINPCRPCKCKCHKCAPNLGEGSPVIFPPNKKVDLMSLTIRKVCVYVDY 292  
QY 294 SHEPDEKVFNMVYDGVENVNAKTKPREQVNSTVNVSVLTVLHODWLNKGEYKCKVSNK 353  
DB 293 SEDPRDOVISWFWNVNVEVHTAQOTQTHREDYNSTIRVSALEPIQHODWMSKEFKCKVSNK 352  
QY 354 ALPAPIETKSKAGQPREPOVYTLPPSRREMTKNQVSLTCLVYGFPSDIAVEMESGQ 413  
DB 353 DLPSPRIETKSKIGLVRAPOVYTLPPRAEQLSKRDKVSLTCLVYGFNGDLSVEMTSNGH 412  
QY 414 PENNYKTPPYLDSDGSFFLYSKLTVDKSRWQGNVSCSVNHEALHNHYTKSLSPG 473  
DB 413 TEENYKTPPYLDSDGSFFLYSKLTVDKSRWQGNVSCSVNHEALHNHYTKSLSPG 472  
QY 474 K 474  
DB 473 K 473

## RESULT 7

Q9R1A4 PRELIMINARY; PRT; 437 AA.  
AC Q9R1A4;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Gamma1 heavy chain of Mab7 (Fragment).  
GN IGH-4.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;  
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal antibody (Mab 7, its light and heavy chains) and construction of a  
RT single chain antibody (scFv).";  
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF152372; AAD40243.1; -  
DR HSSP; P01842; 7FAB.  
DR MGI; MGI:96446; Igh-4.  
DR InterPro; IPR007110; Ig\_Like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 4.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS0835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; 1.  
FT NON\_TER 1  
FT NON\_TER 437  
SQ SEQUENCE 437 AA; 48142 MW; 5C3A7BB3BE7D697C CRC64;

Query Match 61.3%; Score 1541.5; DB 11; Length 437;  
Best Local Similarity 63.0%; Pred. No. 9.7e-119;  
Matches 288; Conservative 68; Mismatches 78; Indels 23; Gaps 7;

QY 21 VQLLESGGGLVQPGSGSLRSCAASGFTFSNAMSVMVRAPGKGLEWVAISASGSHSTYLA 80  
DB 1 VQLLESGGGLVQPGSGSLRSCAASGFTFSNAMSVMVRAPGKGLEWVAISASGSHSTYLA 59  
QY 81 DSVKGRFTISRDNKNTLYLQMSLRADETAVYCAKREVTMIIVNLNGFD-YWGQGTIR 139  
DB 60 DSVKGRFTIYKDKDRNLIQLQMSLRSEDTAMYYCAR-----GDYSAYWGPQT 108  
QY 140 VTVMWNSGALTSVHTPRAVLQSSGLVSLSSVTVVPSSLSGTOTYICNVNHRKPSNTKYDK 199  
DB 109 VTVMWNSGALTSVHTPRAVLQSSGLVSLSSVTVVPSSLSGTOTYICNVNHRKPSNTKYDK 168  
QY 200 VQLLESGGGLVQPGSGSLRSCAASGFTFSNAMSVMVRAPGKGLEWVAISASGSHSTYLA 257  
DB 169 VQLSD-LYTLSSSVTVPPSSVTPSSEYTCNVNHRKPSNTKYDKKIVPRDGG-----CKPCCT 223  
QY 258 APPELLGSPVFLFPKPKDTLMISRTPEVTCVYVDYSHEDPEKVFNMVYDGVENVNAKTK 317  
DB 224 VPEV--SSVPIFPKPKADVLTILTPKVTNVVVDISKDDEVOFSMEVDDVEVHTAQOT 280  
QY 318 PREQVNSTVNVSVLTVLHODWLNKGEYKCKVSNKALPAPIETKSKAGQPREPOVYTL 377  
DB 281 PREQVNSTVNVSVLTVLHODWLNKGEYKCKVSNKALPAPIETKSKAGQPREPOVYTL 340  
QY 378 LPPSRREMTKNQVSLTCLVYGFPSDIAVEMESGQPREPOVYTLPPYLDSDGSFFLYSKL 437  
DB 341 IPPKEDQAKVAVSLTCLMCTITFPREDITVEQNMNGQDAENYKKNQPIIMDTGSGFFVYSKL 400  
QY 438 TVDKSRWQGNVSCSVNHEALHNHYTKSLSPG 474  
DB 401 NVOKSNMEAGNTFTCSVLHGLHNHHTKSLNSHPGK 437

## RESULT 8

Q9D8L4 PRELIMINARY; PRT; 473 AA.  
ID Q9D8L4

AC 09D814:  
 DT 01-JUN-2001 (TREMBlrel. 17, Created)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE 1810060009Rik protein.  
 GN IGH-1 OR 1810060009Rik.  
 OS Mus musculus (Mouse)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Pancreas;  
 RX MEDLINE=21085660; PubMed=11217851;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.I.,  
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Glass C., King B., Kochila H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
 RA Schiml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamlya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mommaerts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilmink L.,  
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,  
 RA Hayashizaki Y.,  
 RT "Functional annotation of a full-length mouse cDNA collection."  
 RL Nature 409:685-690(2001).  
 DR EMBL: AK007918; BAB25349.1;  
 DR HSSP: P01842; 7FAB.  
 DR MGD: MGI:96443; Igh-1.  
 DR InterPro: IPR007110; Iq-1like.  
 DR InterPro: IPR003006; Iq\_MHC.  
 DR InterPro: IPR003596; Iq\_v.  
 DR Pfam: PF00047; Iq; 4.  
 DR SMART: SM00406; Iq; 1.  
 DR PROSITE: PS50835; Iq\_LIKE; 4.  
 DR PROSITE: PS00290; Iq\_MHC; 1.  
 SQ SEQUENCE 473 AA; 51699 MW; 9DED57A514475FBB CRC64;  
 Query Match 60.1%; Score 1511.5; DB 11; Length 473;  
 Best Local Similarity 57.1%; Pred. No. 3.2e-116;  
 Matches 277; Conservative 85; Mismatches 100; Indels 23; Gaps 4;  
 QY 1 MEGGLSMFLVAILKGVCEVOLLSEGGGLVPGGSLRLSCAASGFTFSNVAWSVROAP 60  
 DB 1 MEMSWFLFLISGTVAGVHCVOLQSGALVLRPGASVLRKASGVTFTGYINWVKORP 60  
 QY 61 GGLLEWVASIASGSHSTYLADSVKGRFTISRDNSKNTLYIQMNSLRADFTAVYCAKDE 120  
 DB 61 GGLLEWVGELIYPGSGSTYINSEKFKGKATLTTCSSSTAYVHLISLTSSEDSAYVFCARSS 120  
 QY 121 VMIIVVLNGGPD-----YMGCGTRVYVSSASTKGPSPFLAPSSKTSGGTALGLVND 175  
 DB 121 YSYIDL-----FAWYGGLTVTVSAKTTTPSPSYPLAPGSFADQTNMWTGCLVKGTFEP 175  
 QY 176 YRPEPVYVWSNGALTSVHTFPAYVLAQSSGLYSLSSVTVTPSSISCTQTYICNVNHPFN 235  
 DB 176 VTVVWNSGSLSSGVHTFPAYVLOSGLYSLSSVTVTPSSISCTQTYICNVNHPFN 235  
 QY 170 YRPEPVTLTWNSGSLSSGVHTFPALLO-SGLYTLSSVTVTNTWPSQTITCNVAHPASS 228  
 DB 170 YRPEPVTLTWNSGSLSSGVHTFPALLO-SGLYTLSSVTVTNTWPSQTITCNVAHPASS 228  
 QY 236 TVVDKRVKPK-----SCDKHTGCPPCAPPELLGGPSVFLPDKPKPDLMISTPEVTV 289  
 DB 236 TVVDKRVKPK-----SCDKHTGCPPCAPPELLGGPSVFLPDKPKPDLMISTPEVTV 289  
 QY 229 TVVDKRVKPKRVPTONPCPLKRCPCAPADLLGGPSVFLPDKPKIDVIMISLSPVTV 288  
 DB 229 TVVDKRVKPKRVPTONPCPLKRCPCAPADLLGGPSVFLPDKPKIDVIMISLSPVTV 288  
 QY 290 VVDVSHEDPEVKFNNVVDGEVYVNAKTKPREQYNSYRVVSVLTVLHQDIWLNKGEYKCK 349  
 DB 290 VVDVSHEDPEVKFNNVVDGEVYVNAKTKPREQYNSYRVVSVLTVLHQDIWLNKGEYKCK 349  
 QY 289 VVDVSEDDPDVQISMFVNVNVEVHTAQTQTHREDYNSLTAVVLSALPLIQHDMWSGKEFKCK 348  
 DB 289 VVDVSEDDPDVQISMFVNVNVEVHTAQTQTHREDYNSLTAVVLSALPLIQHDMWSGKEFKCK 348

QY 350 VSNKALPAPIEKTISKAKGCPREPOVYTLPPSRREKTNQVSLTCLVKGFTYSDAVEKE 409  
 DB 349 VNNRALPSPIEKTISKPRGPVAPQYVLPAPAEETKKEISLTCLMITFPLPAELAVDWT 408  
 QY 410 SNGCPENNYKTPRPVLDGSGFFYLSKLTVDSSRMQGVNVSQSVNHEALNHHYQKSS 469  
 DB 409 SNGRQENYKNTATVLDSDGSYFMVSKLRVQSKTWERSGLVACSVNHEALNHHYQKSS 468  
 QY 470 LSPGK 474  
 DB 469 RSLGK 473  
 RESULT 9  
 ID 099LC4 PRELIMINARY; PRT; 463 AA.  
 AC 099LC4:  
 DT 01-JUN-2001 (TREMBlrel. 17, Created)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE Similar to RIKEN CDNA 1810060009 gene.  
 GN IGH-4.  
 OS Mus musculus (Mouse)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC Strausberg R.;  
 RL Submitted (Feb-2001) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: BC003435; AAH03435.1;  
 DR HSSP: P01842; 7FAB.  
 DR MGD: MGI:96446; Igh-4.  
 DR InterPro: IPR007110; Iq-4.  
 DR InterPro: IPR003006; Iq\_MHC.  
 DR InterPro: IPR003596; Iq\_v.  
 DR Pfam: PF00047; Iq; 4.  
 DR SMART: SM00406; Iq; 1.  
 DR PROSITE: PS50835; Iq\_LIKE; 4.  
 DR PROSITE: PS00290; Iq\_MHC; 1.  
 SQ SEQUENCE 463 AA; 51007 MW; EAA674C6BBC30783 CRC64;  
 Query Match 59.5%; Score 1495.5; DB 11; Length 463;  
 Best Local Similarity 57.6%; Pred. No. 6.6e-115;  
 Matches 274; Conservative 85; Mismatches 102; Indels 15; Gaps 5;  
 QY 1 MEGGLSMFLVAILKGVCEVOLLSEGGGLVPGGSLRLSCAASGFTFSNVAWSVROAP 60  
 DB 1 MEMIWFLFLISGTVAGVHCVOLQSGALVLRPGASVLRKASGVTFTGYINWVKORP 60  
 QY 61 GGLLEWVASIASGSHSTYLADSVKGRFTISRDNSKNTLYIQMNSLRADFTAVYCAKDE 120  
 DB 61 GGLLEWVGELIYPGSGSTYINSEKFKGKATLTTCSSSTAYVHLISLTSSEDSAYVFCARSS 120  
 QY 121 VMIIVVLNGGPD-----YMGCGTRVYVSSASTKGPSPFLAPSSKTSGGTALGLVND 180  
 DB 121 YSYIDL-----FAWYGGLTVTVSAKTTTPSPSYPLAPGSFADQTNMWTGCLVKGTFEP 175  
 QY 181 VTVVWNSGSLSSGVHTFPAYVLOSGLYSLSSVTVTPSSISCTQTYICNVNHPFN 240  
 DB 181 VTVVWNSGSLSSGVHTFPAYVLOSGLYSLSSVTVTPSSISCTQTYICNVNHPFN 240  
 QY 176 VTVVWNSGSLSSGVHTFPAYVLOSGLYSLSSVTVTPSSISCTQTYICNVNHPFN 234  
 DB 176 VTVVWNSGSLSSGVHTFPAYVLOSGLYSLSSVTVTPSSISCTQTYICNVNHPFN 234  
 QY 241 RVEPKSCDKHTGCP-----CPAPPELLGGPSVFLPDKPKDPMISRPPEVTVVDVSHEDP 298  
 DB 241 RVEPKSCDKHTGCP-----CPAPPELLGGPSVFLPDKPKDPMISRPPEVTVVDVSHEDP 298  
 QY 235 KIVPRDCG-----CKPICVPEV-----SVFIRPKPKDVIITLTPFKVCVVDISKDDP 287  
 DB 235 KIVPRDCG-----CKPICVPEV-----SVFIRPKPKDVIITLTPFKVCVVDISKDDP 287  
 QY 299 EYKFNMYVDGVEYVNAKTKPREQYNSYRVVSVLTVLHQDIWLNKGEYKCKSNKALPAP 358  
 DB 299 EYKFNMYVDGVEYVNAKTKPREQYNSYRVVSVLTVLHQDIWLNKGEYKCKSNKALPAP 358  
 QY 288 EYQFQSWFVDVEVHTAQTQTHREDYNSLTAVVLSALPLIQHDMWSGKEFKCVNSAFAFAP 347  
 DB 288 EYQFQSWFVDVEVHTAQTQTHREDYNSLTAVVLSALPLIQHDMWSGKEFKCVNSAFAFAP 347  
 QY 359 IEKTSKAKGCPREPOVYTLPPSRREKTNQVSLTCLVKGFTYSDAVEKE 418  
 DB 359 IEKTSKAKGCPREPOVYTLPPSRREKTNQVSLTCLVKGFTYSDAVEKE 418

Db 348 IEKISTKGRPKAPQVYTIPTPPKEQMAKVSLTCTMTDFPEPEDITVEMQMGOPAPENY 407  
Qy 419 KTEPVLDSGSFFLYSKLTVDKSRMOQGNVFCSSVMEALHNHYTOKSLSPGK 474  
Db 408 KNTQPIMDTDSGYFYISKLVNOKSMWENAGNFTCSVLHEGLHNHTKESLSHSPGK 463

RESULT 10  
Q99L31 PRELIMINARY: PRT: 468 AA.  
AC Q99L31: 01-JUN-2001 (Tremblrel. 17, Created)  
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)  
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)  
DE Similar to RIKEN CDNA 1810060009 gene.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Strausberg R.;  
RL Submitted (FEB-2001) to the EMBL/Genbank/DBJ databases.  
DR EMBL: BC003878; AA03878.1; -  
DR HSSP: P01842; 7FAB.  
DR InterPro: IPR007110; Ig-1Ike.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003596; Ig\_V.  
DR Pfam: PF00047; Ig; 3.  
DR SMART: SM00406; Igv; 1.  
DR PROSITE: PS50835; IG\_LIKE; 4.  
DR PROSITE: PS00290; IG\_MHC; 1.  
SQ SEQUENCE 468 AA; 51661 MW; 96352328B332ADB CRC64;

Query Match 58.6%; Score 1474; DB 11; Length 468;  
Best Local Similarity 59.2%; Pred. No. 4e-113;  
Matches 280; Conservative 68; Mismatches 113; Indels 12; Gaps 5;

Qy 6 SWL--FLVALIKGVOCEVQLLESGLVOPGSGLSRLSCAAGFTFSNYAMSVROAPGK 63  
Db 4 SMVLEFLMAVYIGVNSEVQLQSGALVRPGASVKLSTAGSFNKKDSLMHNVGQRPQG 63  
Qy 64 LEWVSATISAGSHSTYLDVSKGRFTISDNKNTLYLQMSNLRAEDTAIVVYCANDEVTM 123  
Db 64 LEWIGWIDPEDEGKTKYAPKFDKATLTADTSSNTAYLQSLSTSDTAIYCARV----- 118  
Qy 124 IVNLNGFDYWGQGTTRVTVSSASTKGPVFLAPSSKSTSGTAALGCLVADYPEPYT 183  
Db 119 -LLGCGYDYWGQGTITTVSSAKTTAPSVYPLAVYCGDTTSSVTLGCLVAGTPEPYTL 177  
Qy 184 SWNSGALTSGVHTFPAVLQSSGLYSLSSVYTPSSSLGTQTYICNVNHRKPSNTYVDKKE 243  
Db 178 TWNSGSLSSGVHTFPAVLQSD-LYTLSSSVYTPSSSITCNVAHPASTYVDKKE 236  
Qy 244 PKSCDKHTCTPR--CPAPELLGSPVFLFPPKPKDTLMISKTPEYTCYVVDVSHDEPYK 301  
Db 237 PRG-PTIKPCPCPKCPAPNLLGSPVFLFPPKIKDVLMISLSPMTCCVVDVSEDDPVQ 295  
Qy 302 FNNYVDGEVHNATKPREEOYNSTYRVSVLYTLHODMLNGKEKCVNKKALPAPLER 361  
Db 296 ISWVNVNVEVLTATQTHREDYNSTLRVVSALPIOHODMMSGKEKCKVNNKALPAPLER 355  
Qy 362 TISKAGQPREPOVYTLPPSREEMTKNOVSLTCLVKGYFSPDAVEMESNQPENNYKTT 421  
Db 356 TISKPGSVRAPOVYVLPPEEEMTKKQVTLTCVTDPEMDIYVEMTNKKTLENTYKNT 415  
Qy 422 PPLVDSGGSFFLYSKLTVDKSRMOQGNVFCSSVMEALHNHYTOKSLSPGK 474  
Db 416 EPVLDSGSYFMYSKLRYEKKMVERNSYSCSVYHEGLHNHTTKFSRTPGK 468

RESULT 11  
Q99L25

ID 099L25 PRELIMINARY: PRT: 473 AA.  
AC Q99L25:  
DT 01-JUN-2001 (Tremblrel. 17, Created)  
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)  
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)  
DE Similar to RIKEN CDNA 1810060009 gene.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Strausberg R.;  
RL Submitted (FEB-2001) to the EMBL/Genbank/DBJ databases.  
DR EMBL: BC003888; AA03888.1; -  
DR HSSP: P01842; 7FAB.  
DR InterPro: IPR007110; Ig-1Ike.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003596; Ig\_V.  
DR Pfam: PF00047; Ig; 3.  
DR SMART: SM00406; Igv; 1.  
DR PROSITE: PS50835; IG\_LIKE; 4.  
DR PROSITE: PS00290; IG\_MHC; 1.  
SQ SEQUENCE 473 AA; 52449 MW; BE989B7986DA155 CRC64;

Query Match 57.5%; Score 1446.5; DB 11; Length 473;  
Best Local Similarity 56.4%; Pred. No. 7.5e-111;  
Matches 274; Conservative 75; Mismatches 112; Indels 25; Gaps 5;

Qy 1 MEFGSLWFLVALIKGVOCEVQLLESGLVOPGSGLSRLSCAAGFTFSNYAMSVROAP 60  
Db 1 MEMSWVLEFLFSLVTTGVSQVLOQSDALELVKPGASVYKICKVGYFTDHTIMVQRP 60  
Qy 61 GKGLEWVSATISAGSHSTYLDVSKGRFTISDNKNTLYLQMSNLRAEDTAIVVYCANDE 120  
Db 61 EGLEWVGYITPRPGSTYVNEKFKGKATLTADKSSSTAYLQMSNLSTSDSVVCFCSR--- 117  
Qy 121 VTMTVLNGG-----FDYWGQGTTRVTVSSASTKGPVFLAPSSKSTSGTAALG 170  
Db 118 -----GGSITYGGLYFDYWGQGTITTVSSAKTTAPSVYPLAVYCGDTTSSVTLG 169  
Qy 171 CLVADYPEPYTSMNSGALTSGVHTFPAVLQSSGLYSLSSVYTPSSSLGTQTYICNVN 230  
Db 170 CLVGYPEPYTLTWNSGSLSSGVHTFPAVLQSD-LYTLSSSVYTPSSSITCNVA 228  
Qy 231 HKPSNTYVDKVERKSCDKHTCTPR--CPAPELLGSPVFLFPPKPKDTLMISKTPEYTC 288  
Db 229 HPASTYVDKKTIERG-PTIKPCPCPKCPAPNLLGSPVFLFPPKIKDVLMISLSPMTCC 287  
Qy 289 VVDVSHDEPYKENVYVDGEVHNATKPREEOYNSTYRVSVLYTLHODMLNGKEYKC 348  
Db 288 VVDVSEDDPVQISMVFNNEVLTATQTHREDYNSTLRVVSALPIOHODMMSGKEKCK 347  
Qy 349 KVSNNKALPAPLEKTIISAKQOPREPOVYTLPPSREEMTKNOVSLTCLVKGYFSPDAVEM 408  
Db 348 KVNKKALPAPLEKTIISAKQSVRAPOVYVLPPEEEMTKKQVTLTCVTDPEMDIYVEM 407  
Qy 409 ESNQPENNYKTPPEVLDSDGSFFLYSKLTVDKSRMOQGNVFCSSVMEALHNHYTOKSL 468  
Db 408 TNNKTELENTYNTPEVLDSDGSYFYISKLRYEKKMVERNSYSCSVYHEGLHNHTTKSF 467  
Qy 469 SLSPGK 474  
Db 468 SRTPGK 473

RESULT 12  
Q983H6 PRELIMINARY: PRT: 474 AA.  
AC Q983H6:  
DT 01-JUN-2002 (Tremblrel. 21, Created)  
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)  
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)



DE Hypothetical 51.7 kDa protein.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Strausberg R.;  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC025447; AAH25447.1; -  
 DR InterPro: IPR000345; CYC\_heme\_bind.  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_V.  
 DR Pfam: PF00047; Ig\_3.  
 DR SMART; SM00406; IgV\_1.  
 DR PROSITE; PS00190; CYTOCHROME\_C\_1.  
 DR PROSITE; PS00835; IG\_LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 474 AA; 51748 MW; 8608B57C6CD2874A CRC64;

Query Match 56.2%; Score 1414; DB 11; Length 474;  
 Best Local Similarity 55.7%; Pred. No. 3,6e-108;  
 Matches 268; Conservative 79; Mismatches 120; Indels 14; Gaps 4;

OY 1 MEFGLSWLFLVAALKGVOCENVOLLESGGGLVDPGSLRISCAAGFTSNVMSVNRQAP 60  
 DB 1 MEMPILFLFLSVTGVSQVOLLQSGPELVKFGASVSKISCRASGAFSKSMWNVKKRP 60  
 OY 61 GKGLEWNASIASGSHSTLADSVKGRFTSRDMSNTLYLQMSLRAREPTAYVCAKDE 120  
 DB 61 GKGLEWIGRITPGDGDTHSGKFGKAKLTADKSSVTAFQLTSLSEDSAVYFCARSD 120  
 OY 121 VTMIVVLNGEDYMGOGTRVTVSSATKGPVFLAPSSKSTSGGTAALGCLVKDYFPEP 180  
 DB 121 -----YGDYFDMDGQGAFTVTVSSAKTTPPSYPLAPGGGDTTSGSVTLGCLVKGFPPS 174  
 OY 121 VTVSNNSGALTSNGVTPRAVLQSSGLYSLSSVTVPPSSLTGQTYICNVNHRKPSNTKDK 240  
 DB 175 VTVSNNSGSLSSVHTFPALLO-SGLYTMSSSVTVPSSTWPSQTYWCVSAHFASSSTYVDK 233  
 OY 241 RPEKSCDKT-HITCP-----CPAPELLGSPVSLFPKPKDITLMISTPREVTCVVNV 293  
 DB 234 KLEPGSPITSTIPCPCKECHKCPANLEGGPSVFLFPNNIDVLMISTLPKVTCCVVNV 293  
 OY 294 SHEDEVEFNNVYDSEVYHNATKPREQYNSTYRVSVLTVLHODWLNKGEYKCKVSNK 353  
 DB 294 SEDDDVQISWVNVNVEYHTAQTQHNREDYNTIIVYSALPIQHDWMSGKFKCKVNNK 353  
 OY 354 ALPADIEKTSKAKQPREPOVYLLPSSHEMTKNQVSLTCLVGFYPSDIAVEMESNGQ 413  
 DB 354 DLPSPIEKTSKIKILVAPQYIILPPAEQLSRKDVSLTCLVGFNPEDISEVETSNHG 413  
 OY 414 PENNKYTPRVLDSCGSFELYSKLVDSRMQGVNFGSVNHEALHNHYTOKSLSLSPG 473  
 DB 414 TEENKDTAPVLDSDGSYFYISKLDIKTSKWKERTDSCNVNHEGLKNYILKTTISRSPG 473  
 OY 474 K 474  
 DB 474 K 474

RESULT 13  
 O95M34 PRELIMINARY: PRT; 337 AA.  
 AC O95M34;  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE Immunoglobulin gamma 1 heavy chain constant region (Fragment).  
 GN IGHC1.  
 OS Equus caballus (Horse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
 OX NCBI\_TaxID=9796;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Wagner B.;  
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-98383416; PubMed-9717671;  
 RX Wagner B., Overesch G., Sheoran A., Holmes M., Richards C.,  
 RT Leibold W., Radbruch A.;  
 RT "Organization of the equine immunoglobulin heavy chain constant region  
 genes. III. Alignment of c-mu, c-gamma, c-epsilon and c-alpha genes."  
 RL Immunobiology 199;105-119(1998).  
 DR EMBL; AJ300675; CAC44624.1; -  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003597; Ig\_C1.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR Pfam: PF00047; Ig\_2.  
 DR SMART; SM00407; IgC1\_2.  
 DR PROSITE; PS00835; IG\_LIKE; 3.  
 DR PROSITE; PS00290; IG\_MHC; 2.  
 FT NON\_TER  
 SQ SEQUENCE 337 AA; 37438 MW; A60BF2B01DEFD1F6 CRC64;

Query Match 50.3%; Score 1263.5; DB 6; Length 337;  
 Best Local Similarity 68.9%; Pred. No. 5,8e-96;  
 Matches 233; Conservative 44; Mismatches 52; Indels 9; Gaps 3;

OY 145 ASTKPSVPLAPSSKSTSGTALGCLVKDYFPEPVTVSNISGALTSGVHFPVLIQSS 204  
 DB 1 ASTAPKVFALAPGCGTSDSTVALGCLVSGFPEPVKASINSGLTSVHTFPVLIQSS 60  
 OY 205 GLYSLSVTVTPSSSLGTQTYICNVNHRKPSNTKVDKRVPR-----KSCDKHTGPPCPA 258  
 DB 61 GLYSLSVMTVASTMTSETIYICNVNHAASNFKVDKRIEP...EDNHQKVDMS-KCPKCPA 119  
 OY 259 PELLGSPVFLFPKPKDITLMISTPREVTCVVNVSDHEDPIYKFNMYDGVENVHNAKTP 318  
 DB 120 PELLGSPVFIIPPNNKDTLMTIRPEVTCVVNVSDQENPIYKFNMYDGVENVHNAKTP 179  
 OY 319 REQYNSTYRVSVLTVLHODWLNKGEYKCKVSNALPAP...EKTISKAKQPREPOVYLL 378  
 DB 180 KEQFQSTYRVSVLTVLHODWLNKGEYKCKVNNQALPOP...ERTTKTGRSGQEPQVYLL 239  
 OY 379 PSREEMTQVSLTCLVGFYPSDIAVEMESNGQP--ENIKYTPRVLDSDGSFELYSK 436  
 DB 240 APHPBELSKSKSVCLVYDFYLPRELINIMQSNQGELETIKYSTTQAQSDSDGSFELYSK 299  
 OY 437 LTVDSRMQGVNFGSVNHEALHNHYTOKSLSLSPG 474  
 DB 300 LSVDRRMQGVNFGSVNHEALHNHYTOKVNSKNPK 317

RESULT 14  
 O96P08 PRELIMINARY: PRT; 701 AA.  
 ID O96P08;  
 AC O96P08;  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE Factor VII active site mutant immunoglobulin.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homindidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-21477448; PubMed-11593034;  
 RA Hu Z., Garen A.;  
 RT "Targeting tissue factor on tumor vascular endothelial cells and tumor  
 cells for immunotherapy in mouse models of prostatic cancer."

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RL Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL: AF212774; AK58686.1; -
DR HSSP: P00761; IAN1
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000742; EGF_2.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR001438; EGF_II.
DR InterPro: IPR006209; EGF_like.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003597; Ig_c1.
DR InterPro: IPR001254; Ser_protease_Try.
DR InterPro: IPR000294; VltK_dep_GLA.
DR Pfam: PF00008; EGF_2.
DR Pfam: PF00594; gla; 1.
DR Pfam: PF00047; Ig; 2.
DR Pfam: PF00089; trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00010; EGFBLD.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00179; EGF_CA; 1.
DR SMART: SM0069; GLA; 1.
DR SMART: SM00407; IGCL; 1.
DR SMART: SM00020; TRYP_SPEC; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; 1.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS01186; EGF_2; 1.
DR PROSITE: PS01187; EGF_CA; 1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE: PS50835; IG_LIKE; 2.
DR PROSITE: PS00290; IG_MHC; 1.
DR PROSITE: PS50240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; 1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
DR EGF-like domain; Hydrolase; Protease; Serine protease.
KW SEQUENCE 701 AA; 77826 MW; 94AC6CEB42CC9292P CRC64;
SQ

Query Match 50.0%; Score 1257; DB 4; Length 701;
Best Local Similarity 99.1%; Pred. No. 5.7e-95;
Matches 230; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 243 EPKSCDKHTHTCPPCAPPELLGGPSVFLFPPRKQDTLMISRTPEYTCVVDVSHEDPEVKF 302
DB 470 EPKSCDKHTHTCPPCAPPELLGGPSVFLFPPRKQDTLMISRTPEYTCVVDVSHEDPEVKF 529

QY 303 NMVYDGVNNAKTKRPREQYNSTYRVYSLTLYLHODMLNGKEYCKVSNKALPAPIEKT 362
DB 530 NMVYDGVNNAKTKRPREQYNSTYRVYSLTLYLHODMLNGKEYCKVSNKALPAPIEKT 589

QY 363 ISKAKGQRPQVYTLPPSRREMTKNQVSLCLVKGFPSPDIAYEWESNGPPENNYKTTTP 422
DB 590 ISKAKGQRPQVYTLPPSRREMTKNQVSLCLVKGFPSPDIAYEWESNGPPENNYKTTTP 649

QY 423 PVLDSGSEFLYSLKLYDKSRMOQGNVFCSCVMHEALHNHYTOKSLSLSPGK 474
DB 650 PVLDSGSEFLYSLKLYDKSRMOQGNVFCSCVMHEALHNHYTOKSLSLSPGK 701

RESULT 15
Q96BB9 PRELIMINARY; PRT; 597 AA.
AC Q96BB9.
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
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RN [1]
SEQUENCE FROM N.A.
RP Tissue-B-cell;
RA Strausberg R.;
Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC015760; AAH15760.1; -
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 5.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 5.
DR PROSITE: PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 597 AA; 65039 MW; 4FCA3AD8CE26309P CRC64;

Query Match 42.2%; Score 1061.5; DB 4; Length 597;
Best Local Similarity 40.5%; Pred. No. 6.1e-79;
Matches 240; Conservative 73; Mismatches 147; Indels 133; Gaps 17;

QY 1 MEFGLSWFLVAIIKGVQCEVQLLESGGGLVQPGSLRLSCAASGFTPESNYAMSVNQAP 60
DB 1 MEFGLSWFLVAIIKGVQCEVQLLESGGGLVQPGSLRLSCAASGFTPESNYAMSVNQAP 60

QY 61 GKLEWVSAISAGSHSTYLADSVKGRFTISRDNSKNTLYIQMNSLRADETAVYYCAND-- 118
DB 61 GKLEWVSAISAGSGSTFYADSVKGRFTISRDNSRDTLYIQMNSLRADETAVYYCANDPR 120

QY 119 -----REVTVIIVLVNGFPDYWGQSTRVTVSASIKGVSFPLAPSSKSTSG-GTAA 168
DB 121 GYSASGNYTR-----DYGQGTLYTVSSGSAAPTLPLPVSCENSPDTSVA 169

QY 169 LGCLVKDYFPEPVTVSW--NSGALTSGVTHFPAVLQSSGLTSLSSVTPVSSSL--GTQT 224
DB 170 VGCLAQDFLPDSTIFPSMKTKKNSDISIRGPPSVLR-GGKYAAISQVILPESKDVMOGTDE 228

QY 225 Y-ICNVNHNKPSN-----TKVDKRVPEKS-----CDKHTGCP-- 254
DB 229 HVCVKVQHPRNCKEKNVPLPVIAELPRKVSFVFPDQFPGNPKRSKLICQATGTFSPROI 288

QY 255 -----PCPAPPELLGGPS----- 266
DB 289 QVSWLRBQKQVSGVTTDQVOAEAKESQPTYYKVTSTLTIKESDMLQSOMFTCVNDRGL 348

QY 267 -----VFLFPPRKQDTLMISRTPEYTCVVDVSHEDPEVKFNNYVD 307
DB 349 TFGQNASMCVPDDDTAIRVAIRPPS-FASIFLTKSRKTLCTLVLDLTYYD-SVITSMTRQ 406

QY 308 GVEVYHNAKTKRPREQYNSTYRVYSLTLYLHODMLNGKEYCKVSNKALPAPIETISKAK 367
DB 407 NGEAVKTKTNTISESHPNATFSAVGEASICEDDMNSGERFTCTVTHTDLPSPLKQITSPK 466

QY 368 GQP-REPOVYTLPPSRREMT-KNQVSLCLVKGFPSPDIAYEWESNGOP--ENNYKTTTP 423
DB 467 GVALHRPDVYTLPPARDELNIRESATITCLVTGSPADVFYQMMQKGPOLSPPEKYVVSAP 526

QY 424 VLD--SDGSFELYSLKLYDKSRMOQGNVFCSCVMHEALHNHYTOKSLSLSPGK 474
DB 527 MPEQAPRGYFAHSLITVSEEMNTGELYTCVVAHEALPNVTERTYDKSKGK 579
```

Search completed: September 12, 2003, 13:03:27  
Job time : 85.3475 secs

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## OM protein - protein search, using sw model

Run on: September 12, 2003, 12:47:03 ; Search time 20.0847 Seconds  
(without alignments)  
1109.830 Million cell updates/sec

Title: US-09-848-832-3  
Predict score: 2514  
Sequence: 1 MEEGLSWLFLVAILKGYQE.....MHEALHNHYTKSLSLSPGK 474

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysts of the total score distribution.

## SUMMARIES

Result No.	Score	Query % Match	Length	ID	Description
1	1758	69.9	330	1	GC1_HUMAN
2	1610	64.0	326	1	P01857 homo sapien
3	1599.5	63.6	327	1	GC4_HUMAN
4	1231.5	49.0	323	1	GC_RABIT
5	1210.5	48.2	329	1	GC2_CAVPO
6	1162	46.2	290	1	GC3_HUMAN
7	1155	45.9	326	1	GC1_RAT
8	1150	45.7	329	1	GC3_MOUSE
9	1145	45.5	324	1	GC1_MOUSE
10	1144.5	45.5	333	1	GC8_RAT
11	1140	45.3	393	1	GC1M_MOUSE
12	1139	45.3	398	1	GC3M_MOUSE
13	1129	44.9	330	1	GC4A_MOUSE
14	1127.5	44.8	329	1	GC1_MOUSE
15	1126.5	44.8	335	1	GCAB_MOUSE
16	1124	44.7	399	1	GCAM_MOUSE
17	1115	44.4	322	1	GC4_RAT
18	1085	43.0	336	1	GC8_MOUSE
19	1080	43.0	405	1	GC8M_MOUSE
20	577	23.0	117	1	HV3C_HUMAN
21	515.5	20.5	116	1	HV05_CARAU
22	486.5	19.4	429	1	EPIC_RAT
23	486	19.3	428	1	EPIC_HUMAN
24	485.5	19.3	136	1	HV16_MOUSE
25	479.5	19.1	421	1	HV3G_HUMAN
26	471	18.7	421	1	EPIC_MOUSE
27	466	18.5	117	1	HV54_MOUSE
28	461	18.3	117	1	HV55_MOUSE
29	460	18.3	121	1	HV3J_HUMAN
30	459	18.3	144	1	HV26_MOUSE
31	454	18.1	144	1	HV59_MOUSE
32	454	18.1	142	1	HV01_RAT
33	452	18.0	455	1	MUC_MOUSE

## ALIGNMENTS

34	450.5	17.9	458	1	MUC_RABIT
35	450	17.9	117	1	HV58_MOUSE
36	449	17.9	115	1	P01765 homo sapien
37	445	17.7	454	1	MUC_HUMAN
38	444	17.7	119	1	HV3I_HUMAN
39	443.5	17.6	122	1	HV3H_HUMAN
40	442	17.6	476	1	MUCM_MOUSE
41	441	17.5	117	1	HV53_MOUSE
42	440.5	17.5	479	1	MUCM_RABIT
43	438.5	17.4	115	1	HV3F_HUMAN
44	438.5	17.4	114	1	HV3B_HUMAN
45	437.5	17.4	126	1	HV3K_HUMAN

  

RESULT 1	
GC1_HUMAN	STANDARD: PRT: 330 AA.
AC P01857	21-JUL-1986 (Rel. 01, Created)
DT	21-JUL-1986 (Rel. 01, Last sequence update)
DT	15-SEP-2003 (Rel. 42, Last annotation update)
DE	Ig gamma-1 chain C region.
CN	IGHG1.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Vertebrate; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX	NCBI_Taxid=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=82274238; PubMed=6287432;
RA	Ellison J.W., Berson B.J., Hood L.E.;
RT	"The nucleotide sequence of a human immunoglobulin C gamma1 gene.";
RL	Nucleic Acids Res. 10:4071-4079(1982).
RN	[2]
RP	SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).
RX	MEDLINE=71064024; PubMed=5489771;
RA	Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,
RT	Waxdal M.J., Edelman G.M.;
RL	"The covalent structure of a human gamma G-immunoglobulin. VII. Amino
RT	acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";
RN	Biochemistry 9:3161-3170(1970).
RP	[3]
RP	SEQUENCE OF 136-329 (EU).
RX	MEDLINE=71064025; PubMed=5530842;
RA	Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,
RT	Edelman G.M.;
RL	"The covalent structure of a human gamma G-immunoglobulin. 8. Amino
RT	acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";
RN	Biochemistry 9:3171-3181(1970).
RP	[4]
RP	SEQUENCE (MYELOMA PROTEIN NIE).
RX	MEDLINE=77070269; PubMed=826475;
RA	Postingsl H., Hilschmann N.;
RT	"The role of antibody structure. The primary structure of a
RT	monoclonal IgG1 immunoglobulin (myeloma protein N.e). III. The
RT	chymotryptic peptides of the H-chain, alignment of the tryptic
RT	peptides and discussion of the complete structure.";
RL	Hope-seyler's Z. Physiol. Chem. 357:1571-1604(1976).
RN	[5]
RP	SEQUENCE (MYELOMA PROTEIN KOL) AND DISULFIDE BONDS.
RX	MEDLINE=83289131; PubMed=6884944;
RA	Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
RT	"Three-dimensional structure determination of antibodies. Primary
RT	structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
RL	Hope-seyler's Z. Physiol. Chem. 364:713-747(1983).
RN	[6]
RP	DISULFIDE BONDS.
RX	MEDLINE=71064027; PubMed=4923144;
RA	Gall W.E., Edelman G.M.;
RT	"The covalent structure of a human gamma G-immunoglobulin. X.

RT Intrachain disulfide bonds.";  
RL Biochemistry 9:3188-3196(1970).  
RN [7]  
RP DISULFIDE BONDS.  
RX MEDLINE-77070267; PubMed-1002129;  
RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;  
RT "Rule of antibody structure. The primary structure of a monoclonal  
RT 1961 immunoglobulin (myeloma protein Nie), I: Purification and  
RT characterization of the protein, the L- and H-chains, the  
RT cyanogen bromide cleavage products, and the disulfide bridges.";  
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).  
RN [8]  
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).  
RX MEDLINE-61208100; PubMed-7235608;  
RA Deisenhofer J.;  
RT "Crystallographic refinement and atomic models of a human P<sub>6</sub> fragment  
RT and its complex with fragment B of protein A from Staphylococcus  
RT aureus at 2.9- and 2.8-A resolution.";  
RL Biochemistry 20:2361-2370(1981).  
CC -1- MISCELLANEOUS: NIE HAS THE GIM(17) ALLOTYPIC MARKER, 97-K, & THE  
CC GIM(1) MARKERS, 239-D & 241-L. KOL & EU SEQUENCES HAVE THE GIM(3)  
CC MARKER & THE GIM (NON-1) MARKERS.  
CC -1- MISCELLANEOUS: NIE ALSO DIFFERS IN THE AMIDATION STATES OF  
CC 35, 116, 198, 269 & 272  
CC -1- MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES  
CC 155, 166, 177, 195, 198, 269, AND 272 AND IN THE ORDER OF RESIDUES  
CC 268-272.  
CC -1- MISCELLANEOUS: KOL ALSO DIFFERS IN THE AMIDATION STATES OF  
CC RESIDUES 198, 267&272.  
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DR EMBL: J00228; AAC82527.1; ALT\_INT.  
DR PIR: A93433; GHU.  
DR PDB: 1FC1; 15-JUL-92.  
DR PDB: 1FC2; 15-JUL-92.  
DR PDB: 1A07; 12-NOV-97.  
DR PDB: 1D5B; 09-FEB-00.  
DR PDB: 1D5I; 09-FEB-00.  
DR PDB: 1D6V; 04-OCT-00.  
DR PDB: 1DN2; 17-MAY-00.  
DR PDB: 1E4K; 06-JUN-01.  
DR PDB: 1FCG; 20-JUL-95.  
DR PDB: 1H2H; 12-JUN-02.  
DR PDB: 1I7H; 08-AUG-01.  
DR PDB: 1IIS; 16-MAY-01.  
DR PDB: 1IIX; 16-MAY-01.  
DR PDB: 1L6X; 10-APR-02.  
DR PDB: 2RCG; 12-NOV-97.  
DR Genew; HGNC:5525; IGHG1.  
DR MIM; 147100; .  
DR GO: GO:0005624; C:membrane fraction; NAS.  
DR GO: GO:0003823; F:antigen binding activity; TAS.  
DR GO: GO:0006955; P:immune response; NAS.  
DR InterPro: IPR007110; Ig-like.  
DR InterPro: IPR003597; Ig-cl.  
DR Pfam: PF00047; Ig; 3.  
DR SMART: SM00407; Igcl; 2.  
DR PROSITE: PS00835; IG\_LIKE; 3.  
DR PROSITE: PS00290; IG\_MHC; 2.  
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;  
KW 3D-structure.  
FT NON\_TER 1 1  
FT DOMAIN 1 98 CH1.  
FT DOMAIN 99 110 HINGE.  
FT DOMAIN 111 223 CH2.

FT	DOMAIN	224	330	CH3.
FT	DISULFID	27	83	INTERCHAIN (WITH LIGHT CHAIN).
FT	DISULFID	103	103	INTERCHAIN (WITH HEAVY CHAIN).
FT	DISULFID	109	119	INTERCHAIN (WITH HEAVY CHAIN).
FT	DISULFID	112	102	INTERCHAIN (WITH HEAVY CHAIN).
FT	DISULFID	144	204	
FT	DISULFID	144	204	
FT	CARBOHYD	250	308	N-LINKED (GLCNAC. . .).
FT	MOD_RES	180	180	REMOVED POST-TRANSLATIONALLY.
FT	MOD_RES	330	330	K -> R (IN GIM(3) MARKER).
FT	VARIANT	97	97	/FTID=VAR_003886
FT	VARIANT	239	239	D -> E (IN GIM(NON-1) MARKER).
FT	VARIANT	241	241	/FTID=VAR_003887
FT	VARIANT	241	241	L -> M (IN GIM(NON-1) MARKER).
FT	VARIANT	241	241	/FTID=VAR_003888
FT	STRAND	122	126	
FT	HELIX	130	134	
FT	HELIX	136	137	
FT	STRAND	141	147	
FT	STRAND	157	162	
FT	TURN	163	164	
FT	STRAND	165	166	
FT	TURN	168	171	
FT	STRAND	176	179	
FT	TURN	180	181	
FT	STRAND	182	190	
FT	HELIX	193	197	
FT	TURN	198	199	
FT	STRAND	202	207	
FT	TURN	209	210	
FT	STRAND	215	219	
FT	STRAND	227	227	
FT	STRAND	230	234	
FT	HELIX	238	242	
FT	STRAND	245	256	
FT	STRAND	260	265	
FT	STRAND	270	270	
FT	STRAND	274	276	
FT	STRAND	280	281	
FT	TURN	283	284	
FT	STRAND	287	296	
FT	HELIX	297	301	
FT	TURN	302	303	
FT	STRAND	305	312	
FT	TURN	313	314	
FT	TURN	316	317	
FT	STRAND	320	325	
SO	SEQUENCE	330 AA:	36106 MM:	3770EE106C2FA33D CRC64:
Query Match 99.9%; Score 1758; DB 1; Length 330;				
Best Local Similarity 99.1%; Pred. No. 1.5e-113;				
Matches 327; Conservative 3; Mismatches 0; Indels 0; Gaps 0;				
QY	145	ASTKGPVFPFLAASSKSTSGTALGCLVADYDPPEPTVAMNSGALTSVHTPPAVLOSS	204	
DB	1	ASTKGPVFPFLAASSKSTSGTALGCLVADYDPPEPTVAMNSGALTSVHTPPAVLOSS	60	
QY	205	GLVSLSSVVPSSSLGTQYICNVNHPKPSNTKVDKVEPKSCDKHTPCPCAPPELLGG	264	
DB	61	GLVSLSSVVPSSSLGTQYICNVNHPKPSNTKVDKVEPKSCDKHTPCPCAPPELLGG	120	
QY	265	PSVFLFPKPKDKLTMTSRPEVTCVVVDVSHEDPEVKFNNYVDSGEVHNAAKTRPREQYN	324	
DB	121	PSVFLFPKPKDKLTMTSRPEVTCVVVDVSHEDPEVKFNNYVDSGEVHNAAKTRPREQYN	180	
QY	325	STYRVSVLVTLVQDMLNGKEYCKCKSNKAALPARIETISKAKGQPREPQVYTLPPSRREE	384	
DB	181	STYRVSVLVTLVQDMLNGKEYCKCKSNKAALPARIETISKAKGQPREPQVYTLPPSRREE	240	
QY	385	MTRKQVSLTCLVAGFYPSDIAVEMESNGQPENNYKTPPYLDSGSPFLYSLKTLVDKSRW	444	
DB	241	LTRKQVSLTCLVAGFYPSDIAVEMESNGQPENNYKTPPYLDSGSPFLYSLKTLVDKSRW	300	

OY 445 OOGNVEGCVMEALHNHYTOKSLSPGK 474  
 DB 301 OOGNVEGCVMEALHNHYTOKSLSPGK 330

RESULT 2  
 GC2\_HUMAN STANDARD: PRT: 326 AA.  
 AC P01859;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Ig gamma-2 chain C region.  
 GN IGHG2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE OF 2-326 FROM N.A.  
 RX MEDLINE=82197621; PubMed=6804948;  
 RA Ellison J.W., Hood L.E.;  
 RT "Linkage and sequence homology of two human immunoglobulin gamma  
 heavy chain constant region genes.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).  
 RN [2]  
 RP SEQUENCE OF 88-115 FROM N.A.  
 RX TISSUE=Fetal liver;  
 RA MEDLINE=83001943; PubMed=6811139;  
 RA Takahashi N., Ueda S., Obata M., Nikaide T., Nakai S., Honjo T.;  
 RT "Structure of human immunoglobulin gamma genes: implications for  
 evolution of a gene family.";  
 RL Cell 29:671-679(1982).  
 RN [3]  
 RP SEQUENCE OF 99-177 AND 310-326 FROM N.A.  
 RX TISSUE=Fetal liver;  
 RA MEDLINE=84235992; PubMed=6329676;  
 RA Krawinkel U., Rabbits T.H.;  
 RT "Comparison of the hinge-coding segments in human immunoglobulin gamma  
 heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass  
 genes.";  
 RL EMBO J. 1:403-407(1982).  
 RN [4]  
 RP SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).  
 RX MEDLINE=81007873; PubMed=6774012;  
 RA Wang A.-C., Tung E., Fudenberg H.H.;  
 RT "The primary structure of a human IgG2 heavy chain: genetic,  
 evolutionary, and functional implications.";  
 RL J. Immunol. 125:1048-1054(1980).  
 RN [5]  
 RP SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).  
 RX MEDLINE=80001357; PubMed=113060;  
 RA Connell G.E., Parr D.M., Hofmann T.;  
 RT "The amino acid sequences of the three heavy chain constant region  
 domains of a human IgG2 myeloma protein.";  
 RL Can. J. Biochem. 57:758-767(1979).  
 RN [6]  
 RP SEQUENCE OF 238-275 (ZIE).  
 RX MEDLINE=80114419; PubMed=118920;  
 RA Hofmann T., Parr D.M.;  
 RT "A note of the amino acid sequence of residues 381-391 of human  
 immunoglobulin gamma chains.";  
 RL Mol. Immunol. 16:923-925(1979).  
 RN [7]  
 RP REVISIONS TO 25; 59; 60 AND 264-268 (ZIE).  
 RA Hofmann T., Parr D.M.;  
 RL Submitted (MAR-1980) to the PIR data bank.  
 RN [8]  
 RP SEQUENCE OF 1-121 (DOT).  
 RX MEDLINE=95255298; PubMed=7737190;  
 RA Stopnini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;  
 RT "Characterization of the two unique human anti-flavin monoclonal  
 immunoglobulins.";

RL Eur. J. Biochem. 228:886-893(1995).  
 RN [9]  
 RP DISULFIDE BONDS.  
 RX MEDLINE=72033500; PubMed=4940472;  
 RA Milstein C., Frangione B.;  
 RT "Disulphide bridges of the heavy chain of human immunoglobulin G2.";  
 RL Biochem. J. 121:217-225(1971).  
 RN [10]  
 RP DISULFIDE BONDS.  
 RX MEDLINE=69064124; PubMed=5782707;  
 RA Frangione B., Milstein C., Pink J.R.L.;  
 RT "Structural studies of immunoglobulin G.";  
 RL Nature 221:145-148(1969).  
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 DR EMBL: J00230; AAB59393.1; .  
 DR PIR: A93906; G2HU.  
 DR HSSP: P01857; 1RCL.  
 DR GeneW: HGNC:5526; IGHG2.  
 DR MIM: 147110; .  
 DR GO: GO:0005624; C:membrane fraction; NAS.  
 DR GO: GO:0003823; F:antigen binding activity; TAS.  
 DR GO: GO:0006955; P:immune response; NAS.  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003597; Ig-cl.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR Pfam: PF00047; Ig; 3.  
 DR SMART: SM00407; IGc1; 2.  
 DR PROSITE: PS00835; IG\_LIKE; 3.  
 DR PROSITE: PS00290; IG\_MHC; 2.  
 KW Immunoglobulin domain; Immunoglobulin C region.  
 FT NON\_TER 1 1  
 FT DOMAIN 1 98 CH1.  
 FT DOMAIN 99 110 HINGE.  
 FT DOMAIN 111 219 CH2.  
 FT DOMAIN 220 326 CH3.  
 FT DISULFID 14 14 INTERCHAIN (WITH A LIGHT CHAIN).  
 FT DISULFID 27 83 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 103 103 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 140 200  
 FT DISULFID 246 304  
 FT SITE 246 156  
 FT MOD\_RES 326 326  
 FT VARIANT 60 60  
 FT CONFLICT 109 109 C->S (IN REF. 3).  
 SQ SEQUENCE 326 AA; 35884 MW; 831087BC687BCF9C CRC64;  
 Query Match 64.0%; Score 1610; DB 1; Length 326;  
 Best Local Similarity 91.8%; Pred. No. 2e-103;  
 Matches 303; Conservative 10; Mismatches 13; Indels 4; Gaps 2;

OY 145 ASTKGPVFPPLAPSSKSTSGGTAAGCLVKDYFPEPTVYSNNGALTSGVHFPVAVLOSS 204  
 DB 1 ASTKGPVFPPLAPSSKSTSGGTAAGCLVKDYFPEPTVYSNNGALTSGVHFPVAVLOSS 60

OY 205 GLYSLSSVYTVYSSSLGTQTYICNVNHRPSNKKVKKRPPKSCDCTHPCPPAPPELLGG 264  
 DB 61 GLYSLSSVYTVYSSSLGTQTYICNVNHRPSNKKVKKRPPKSCDCTHPCPPAPPELLGG 116

OY 265 PSVFLPFPKPKDITLISRTPEVTCVAVVDSHPDKFMKYVDGVEVNAKRPPEEQYN 324  
 DB 117 PSVFLPFPKPKDITLISRTPEVTCVAVVDSHPDKFMKYVDGVEVNAKRPPEEQYN 176

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QY 325 STYRVSVLTVLHODMLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREE 384
D 177 STYRVSVLTVLHODMLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREE 236
QY 385 MTRKNOVSLTCLVAGFYPSDIAVEMESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 444
D 237 MTRKNOVSLTCLVAGFYPSDIAVEMESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 296
QY 445 QGQNVFSCSYMHGALHNHYTKSLSPGK 474
D 297 QGQNVFSCSYMHGALHNHYTKSLSPGK 326

RESULT 3
GC4_HUMAN STANDARD; PRT; 327 AA.
AC P01861;
DT 21-JUL-1986 (Rel. 01, Created)
DY 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-SEP-2003 (Rel. 42, Last annotation update)
GN Ig gamma-4 chain C region.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=63157104; PubMed=6299662;
RA Ellison J.W., Buxbaum J.N., Hood L.E.;
RT "Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";
RL DNA 1:11-18(1981).
RN [2]
RP SEQUENCE OF 1-30 AND 81-326.
RX MEDLINE=70207560; PubMed=4192699;
RA Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;
RT "Human immunoglobulin subclasses. Partial amino acid sequence of the
RL Biochem. J. 117:33-47(1970).
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CC -----
DR EMBL: K01316; AAB59394.1; ALU_INIT.
DR PIR: A90933; GAHU.
DR PDB: IADO; 16-SEP-98.
DR GeneW: HGNC:5528; IGHG4.
DR MIM: 147130.
DR GO: GO:0005624; C:membrane fraction; NAS.
DR GO: GO:0003823; E:antigen binding activity; TAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; I9-1like.
DR InterPro: IPR003597; I9-cl.
DR InterPro: IPR003006; I9-MHC.
DR Pfam: PF00047; I9; 3.
DR SMART: SM00407; I9cl; 2.
DR PROSITE: PS00835; I9_LIKE; 3.
DR PROSITE: PS00290; I9_MHC; 2.
KW Immunoglobulin domain; Immunoglobulin C region; 3D-structure.
FT NON_TER 1 1
FT DOMAIN 1 98 CH1.
FT DOMAIN 99 110 HINGE.
FT DOMAIN 111 220 CH2.
FT DOMAIN 221 327 CH3.
FT DISULFID 14 14 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 63 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 106 106

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FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 141 201
FT DISULFID 247 305
SQ SEQUENCE 327 AA; 35940 MW; 3EDBD811EF208E7A CRC64;

Query Match 63.68; Score 1599.5; DB 1; Length 327;
Best Local Similarly 91.88; Pred. No. 1.1e-102;
Matches 303; Conservative 9; Mismatches 15; Indels 3; Gaps 1;

QY 145 ASTKGPSVPLAPSKSGTGAALGLVDYDEPEPTVYWSNGALTSVHTPEAVYQSS 204
D 1 ASTKGPSVPLAPSKSGTGAALGLVDYDEPEPTVYWSNGALTSVHTPEAVYQSS 60
QY 205 GLYSLSVTVTPSSSLGTQTYICNVNHRPSNTFVDRKVRPEKSCDKHTTCCPAPELLGG 264
D 61 GLYSLSVTVTPSSSLGTQTYICNVNHRPSNTFVDRKVRPEKSCDKHTTCCPAPELLGG 117
QY 265 PSVFLPEPPKPKDMLISRTPEVTCVYVDVSHDEPEVAFNNYVDGVEYHNAKTKPREQYN 324
D 118 PSVFLPEPPKPKDMLISRTPEVTCVYVDVSHDEPEVAFNNYVDGVEYHNAKTKPREQYN 177
QY 325 STYRVSVLTVLHODMLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREE 384
D 178 STYRVSVLTVLHODMLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREE 237
QY 385 MTRKNOVSLTCLVAGFYPSDIAVEMESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 444
D 238 MTRKNOVSLTCLVAGFYPSDIAVEMESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 297
QY 445 QGQNVFSCSYMHGALHNHYTKSLSPGK 474
D 298 QGQNVFSCSYMHGALHNHYTKSLSPGK 327

RESULT 4
GC_RABBIT STANDARD; PRT; 323 AA.
ID GC_RABBIT
AC P01870;
DT 21-JUL-1986 (Rel. 01, Created)
DY 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-SEP-2003 (Rel. 42, Last annotation update)
GN Ig gamma chain C region.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84030930; PubMed=6313520;
RA Bernstein K.E., Alexander C.B., Mage R.G.;
RT "Nucleotide sequence of a rabbit IgG heavy chain from the recombinant
RL F-1 haplotype.";
RN [2]
RP Immunogenetics 18:387-397(1983).
RN [3]
RP SEQUENCE OF 1-128.
RX MEDLINE=76135469; PubMed=1243651;
RA Pratt D.M., Moile L.E.;
RT "Sequence studies on the constant region of the Fd sections of rabbit
RL immunoglobulin G of different allotype.";
RN [4]
RP Biochem. J. 151:337-349(1975).
RN [5]
RP SEQUENCE OF 88-266 FROM N.A.
RX MEDLINE=83299917; PubMed=6193512;
RA Mertens C.L., Moore K.W., Steilmetz M., Hood L., Knight K.L.;
RT "Heavy chain genes of rabbit IgG: isolation of a cDNA encoding gamma
RL heavy chain and identification of two genomic C gamma genes.";
RN [6]
RP Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).
RN [7]
RP SEQUENCE OF 132-161.
RX MEDLINE=70110015; PubMed=5461106;
RA Fruchter R.G., Jackson S.A., Moile L.E., Porter R.R.;
RT "Sequence studies of the Fd section of the heavy chain of rabbit
RL immunoglobulin G.";

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RL Blochem. J. 116:249-259(1970).
RN [5]
RP SEQUENCE OF 129-131 AND 155-322.
RA Hill R.L., Lebovitz H.E., Fellows R.E. Jr., Delaney R.;
RL (in) Kiliander J. (eds.);
RL Gamma globulins, Nobel symp. 3, pp.109-127, Almqvist and Wiksell,
RL Stockholm (1967).
CC -1- MISCELLANEOUS: REF.1 SEQUENCE HAS THE D12 ALLOTYPIC MARKER,
CC 104-THR, AND THE E14 MARKER, 185-THR. REF.3 HAS THE D11 AND E15
CC MARKERS AND REF.5 THE E15 MARKER.
CC -1- SIMILARITY: Contains 3 immunoglobulin-like domains.
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CC -----
DR EMBL: M16426; AAA31289.1; -.
DR PIR: A91749; GHRD.
DR HSSP: P01857; IEC1.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003597; Ig-cl.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig; 2.
DR SMART: SM00407; Igcl; 2.
DR PROSITE: PS50835; IG-LIKE; 3.
DR PROSITE: PS00290; IG_MHC; 1.
RV Immunoglobulin domain: Immunoglobulin C region; Repeat.
FT NON_TER 1
FT DOMAIN 1 96 IG-LIKE 1.
FT 6 213 IG-LIKE 2.
FT DOMAIN 2 222 318 IG-LIKE 3.
FT 104 104 T->M (IN D11 MARKER).
FT VARIANT 185 185 T->A (IN E15 MARKER).
FT CONFLICT 48 48 N->E (IN REF. 2).
FT 71 71 V->VPY (IN REF. 2).
FT CONFLICT 144 144 Q->E (IN REF. 3 AND 4).
FT 173 173 Q->D (IN REF. 5).
FT CONFLICT 187 187 Q->E (IN REF. 3 AND 5).
FT 201 201 N->D (IN REF. 5).
FT CONFLICT 218 218 Q->E (IN REF. 5).
FT 233 233 E->Q (IN REF. 5).
FT CONFLICT 246 246 N->D (IN REF. 5).
FT 256 256 E->G (IN REF. 5).
FT CONFLICT 260 260 N->D (IN REF. 5).
FT 266 266 N->D (IN REF. 5).
FT CONFLICT 280 280 Y->W (IN REF. 5).
FT 284 284 N->S (IN REF. 5).
SQ SEQUENCE 323 AA: 35404 MW: 69E8AA118D579A8B CRC64:
Query Match 49.0%; Score 1231.5; DB 1; Length 323;
Best Local Similarity 70.0%; Pred. No. 1.8e-77;
Matches 229; Conservative 34; Mismatches 57; Indels 7; Gaps 2;

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OY 388 NOVSLTCLYKGFPSDIAVEMESNGCPENNYKTPPEVLDSD3SFLYSLKLVYDKSRMOG 447
DB 237 RVSUTLCHINGFPYDISDISVEMKNGKAEDNYTTTAVLDSD3SYFLINKLSVPTSEMRG 296
OY 448 NVFSCSVMEALHNHYTKSLSPGK 474
DB 297 DVFTCSVMHEALHNHYTKSLSPGK 323

RESULT 5
GC2_CAVPO STANDARD: PRT; 329 AA.
ID GC2_CAVPO
AC P01862;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2 chain C region.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euteria; Rodentia; Hystriocognathi; Caviidae; Cavia.
OX NCBI_Taxid=10141;
RN [1]
RP SEQUENCE OF 1-3.
RA Trischmann T.M.;
RL Submitted (Apr-1975) to the PIR data bank.
RN [2]
RP SEQUENCE OF 4-68.
RX MEDLINE=71058471; PubMed=5538606;
RA Birstein B.K., Hussain Q.Z., Gebra J.J.;
RT "Structure of heavy chain from strain 13 guinea pig
RT immunoglobulin-G(2). 3. Amino acid sequence of the region around the
RT half-cysteine joining heavy and light chains.";
RL Biochemistry 10:18-25(1971).
RN [3]
RP SEQUENCE OF 69-133 AND 312-329.
RX MEDLINE=71058486; PubMed=5538616;
RA Turner K.J., Gebra J.J.;
RT "Structure of heavy chain from strain 13 guinea pig
RT and hinge region cyanogen bromide fragments.";
RL Biochemistry 10:9-17(1971).
RN [4]
RP SEQUENCE OF 134-226.
RX MEDLINE=75036072; PubMed=4429665;
RA Tracey D.E., Gebra J.J.;
RT "Primary structure of the CH2 homology region from guinea pig IgG2
RT antibodies.";
RL Biochemistry 13:4796-4803(1974).
RN [5]
RP SEQUENCE OF 227-311.
RX MEDLINE=75036073; PubMed=4609467;
RA Trischmann T.M., Gebra J.J.;
RT "Primary structure of the CH3 homology region from guinea pig IgG2
RT antibodies.";
RL Biochemistry 13:4804-4811(1974).
RN [6]
RP DISULFIDE BONDS.
RX MEDLINE=71058474; PubMed=4922544;
RA Oliveira B., Lamm M.E.;
RT "Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin.";
RL Biochemistry 10:26-31(1971).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM POOLED SERUM OF STRAIN
CC 13 INBRED GUINEA PIGS.
DR PIR: A94553; G2GP.
DR HSSP: P01842; 7FAB.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003597; Ig-cl.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig; 2.
DR SMART: SM00407; Igcl; 2.
DR PROSITE: PS50835; IG-LIKE; 3.
DR PROSITE: PS00290; IG_MHC; 1.
RV Immunoglobulin domain: Immunoglobulin C region; (i)ycoprotein.

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FT  VARIANT  126  127  OV -> EB (IN ZUC)
FT  DISULFID 134  134  /FTID-VAR_003890.
FT  VARIANT  134  134  P -> L (IN OMM)
FT  VARIANT  139  139  /FTID-VAR_003891.
FT  VARIANT  139  139  F -> Y (IN OMM)
FT  VARIANT  182  182  /FTID-VAR_003892.
FT  VARIANT  182  182  T -> A (IN OMM)
FT  VARIANT  227  227  /FTID-VAR_003893.
FT  VARIANT  227  227  S -> N (IN OMM)
FT  VARIANT  227  227  /FTID-VAR_003894.
FT  VARIANT  227  227  MISSING (IN ZUC)
FT  VARIANT  279  279  /FTID-VAR_003895.
FT  VARIANT  279  279  F -> Y (IN OMM)
FT  SEQUENCE 290 AA: 32331 MW: E69GBC95705B2E46 CRC64:
                               /FTID-VAR_003896.

Query Match      46.2%; Score 1162; DB 1; Length 290;
Best Local Similarity 91.4%; Pred. No. 9e-73;
Matches 212; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

OY  243 EPKSCKTHPCPCAPPELLGSPVFLPPPKFKDLMISRPEVTCVVVDVSHEDPEVKF 302
      |||||  || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB  59 EPKSCDTPPCPCAPPELLGSPVFLPPPKFKDLMISRPEVTCVVVDVSHEDPEYGF 118
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY  303 NMYVDGVEVHNKTRPREBOYSTRVYSLTVLHODMLNGKEYCKVSNKALPAPIEKT 362
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB  119 KMYVGVGVHNKTRPREBOYSTRVYSLTVLHODMLNGKEYCKVSNKALPAPIEKT 178
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY  363 ISKAGOPREPQVYTLPPSREEMTKNOVSLTCLVKGFPYSDIAVEMESNGOPENNYKTP 422
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB  179 ISKTGQPREPQVYTLPPSREEMTKNOVSLTCLVKGFPYSDIAVEMESNGOPENNYKTP 238
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY  423 PVLDSGSEFLYSKLTVDKSRWQGNVFCSSVMEHLNHYTKSLISLSPGK 474
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB  239 PVLDSGSEFLYSKLTVDKSRWQGNVFCSSVMEHLNHYTKSLISLSPGK 290
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 7
GC1_RAT      STANDARD:      PRT;      326 AA.
ID  GC1_RAT
AC  P20759;
DT  01-FEB-1991 (Rel. 17, Created)
DR  01-FEB-1991 (Rel. 17, Last sequence update)
DE  15-JUL-1999 (Rel. 38, Last annotation update)
OS  Ig gamma-1 chain C region.
OC  Rattus norvegicus (Rat).
OC  Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX  NCBI_TaxID=10116;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=89232738; PubMed=3149946;
RA  Bruggemann M.;
RT  "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
RL  Gene 74:473-482(1988).
DR  HSSP: P50017; PS0017.
DR  HSSP: P01842; 7ERD.
DR  InterPro: IPR007110; Ig_1-like.
DR  InterPro: IPR003597; Ig_c1.
DR  InterPro: IPR003006; Ig_MHC.
DR  Pfam: PF00047; Ig_3.
DR  SMART: SM00407; IGc1_2.
DR  PROSITE: PS50835; IG_LIKE; 3.
DR  PROSITE: PS00290; IG_MHC; 1.
KW  Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT  NON_TER  1  1
FT  DOMAIN  1  97  CH1.
FT  DOMAIN  98  112  HINGE.
FT  DOMAIN  113  219  CH2.
FT  DOMAIN  220  326  CH3.
FT  DISULFID 227  82
FT  DISULFID 102  102  INTERCHAIN (WITH A HEAVY CHAIN).
FT  DISULFID 106  106  INTERCHAIN (WITH A HEAVY CHAIN).

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FT  DISULFID 109  109  INTERCHAIN (WITH A HEAVY CHAIN).
FT  DISULFID 111  111  INTERCHAIN (WITH A HEAVY CHAIN).
FT  DISULFID 140  200
FT  DISULFID 246  304
FT  CARBOHYD 176  176  N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ  SEQUENCE 326 AA: 35946 MW: 013BABA5EF49B9DA C1C64;

Query Match      45.9%; Score 1155; DB 1; Length 326;
Best Local Similarity 63.4%; Pred. No. 3.2e-72;
Matches 211; Conservative 52; Mismatches 60; Indels 10; Gaps 4;

OY  145 ASTKSGVPLAPSSKSTSGCTALCLVADYEPPEVTSINSGALTSGVHPEPAVLQSS 204
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB  1 AETLASVYPLAGTALKSNMWTLCGLVKGYPPEVTVTINSGALSSGVHPEPAVLQ-S 59
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY  205 GLYLSSTVYTPSSSLGTQTYICNVNHRKSNTRKVRKVEP:SCDKTHPCPCAPPELLG 264
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB  60 GLYTLTSSVTPSSSTPQVTCNVNHRKSNTRKVRKVEP:SCDKTHPCPCAPPELLG 113
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY  265 ---PSYFLRPPKPKDLMISRPEVTCVVVDVSHEDPEVKIMNYVDGVEVHNKTRPRE 321
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB  114 SEVSVFIEPPKPKDVLTTLPKVCVYVDISQDDPEVNI SMFVDGVEVHNKTRPRE 173
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY  322 QNSTRVYVSLTVLHODMLNGKEYCKVSNKALPAPIEKTISKAGOPREPQVYTLPPS 381
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB  174 QNSTRVYSELPIQLHODMLNGTRFKCKYTSAAFPPIEKTISKAGOPREPQVYTLPPS 233
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY  382 REEMTKNOVSLTCLVKGFPYSDIAVEMESNGOPENNYKTP:PVLDSGSEFLYSKLTVDK 441
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB  234 KEEMTKNEVSIITCMVKGFPYSDIYVEMQNGOQENYKNTP:PMDTDSGSEFLYSKLTVDK 293
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY  442 SRWQGNVFCSSVMEHLNHYTKSLISLSPGK 474
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB  294 ERWQGNVFCSSVMEHLNHYTKSLISLSPGK 326
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 8
GC3_MOUSE    STANDARD:      PRT;      329 AA.
ID  GC3_MOUSE
AC  P22436;
DT  01-AUG-1991 (Rel. 19, Created)
DR  01-AUG-1991 (Rel. 19, Last sequence update)
DE  16-OCT-2001 (Rel. 40, Last annotation update)
OS  Ig gamma-3 chain C region, secreted form.
OC  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=85027161; PubMed=6092053;
RA  Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Matinez H.M.,
RA  Tucker P.W., Bialtner F.R.;
RT  "Structural analysis of the murine Ig3 constant region gene.";
RL  EMBO J. 3:2041-2046(1984).
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CC  -----
DR  EMBL: J00451; -. NOT_ANNOTATED_CDS.
DR  PIR: B02156; G3MSC.
DR  HSSP: P01857; 1FC1.
DR  InterPro: IPR007110; Ig_1-like.
DR  InterPro: IPR003597; Ig_c1.
DR  InterPro: IPR003006; Ig_MHC.
DR  Pfam: PF00047; Ig_3.
DR  SMART: SM00407; IGc1_2.
DR  PROSITE: PS50835; IG_LIKE; 3.

```

DR PROSITE: PS00290; IG\_MHC.1.  
 KM Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;  
 KW Transmembrane; Alternative splicing.  
 FT NON\_TER 1 1  
 FT DOMAIN 1 97 CH1.  
 FT DOMAIN 98 113 HINGE.  
 FT DOMAIN 114 223 CH2.  
 FT DOMAIN 224 327 CH3.  
 SQ SEQUENCE 329 AA; 36228 MW; F45827174182BAD6 CRC64;  
 Query Match 45.7%; Score 1150; DB 1; Length 329;  
 Best Local Similarity 65.0%; Pred. No. 76-72;  
 Matches 215; Conservative 44; Mismatches 68; Indels 4; Gaps 3;  
 QY 146 STKGSPVPLAPSSSTSGGTALCLVNDYFPEPVTVSWNSGALTSGVHTPPAVLQSSG 205  
 DB 1 TTTASVYPLVPGCGDSSSVTLGLCVKGYGPEPVTVKMNYSGLSVGRVSSVLQ -SG 59  
 QY 206 LYSLSVYTPVSSSGTGTTCNVNHNKPSNTKVDKRVKSCDKTHTCF - FCPABELLG 263  
 DB 60 FYSLSLVTPSSSTPSQTVICNVNHPASKTELIRIER - IPKSPSPGSSCPGQNLIG 118  
 QY 264 GPSVPLFPKPKDLMISRTPEVTVVDVSHEDPEVKFNMTYDGVGVNNAKTPREDOY 323  
 DB 119 GPSVPLFPKPKDALMISLTPKVTGVVDVSEDDVDVHVSFWVDNKEVHTANTQPREAOY 178  
 QY 324 NSTVNVSVLYLVHODMLNGKVKCKVSKKALPADIETISKAKQPREPVYTLPPSRE 383  
 DB 179 NSTFNVVALPIODHMKRGEKFKVNNKALPAEIERISPKKRAQCPQVYITPPPRE 238  
 QY 384 EMTKQVSLTCLVKGFPYSDIYEVESNGQPENNKTPPVYDSDGSPFLYSKLVNDSR 443  
 DB 239 QMSKKVSLTCLVTFESEAISVEVERNGELEQDYKNTPIIDSDGTYFLSKLVVDSD 298  
 QY 444 WQGVNESCVAHEALHNHYTQKSLSPGK 474  
 DB 299 WLQGEIFTCVYVHEALHNHYTQKSLSPGK 329  
 RESULT 9  
 GCL\_MOUSE STANDARD: PRT; 324 AA.  
 AC P01868;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ig gamma-1 chain C region secreted form.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=80045036; PubMed=115593;  
 RA Horjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,  
 RT Takahashi N., Mano Y.;  
 RT "Cloning and complete nucleotide sequence of mouse immunoglobulin  
 gamma 1 chain gene.";  
 RL Cell 18:559-568(1979).  
 RN [2]  
 RP SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).  
 RX MEDLINE=80202559; PubMed=6769752;  
 RA Obata M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., Shimizu A.,  
 RT "Immunoglobulin gamma 1 heavy chain gene: structural gene sequences  
 cloned in a bacterial plasmid.";  
 RL Gene 9:87-97(1980).  
 RN [3]  
 RP SEQUENCE OF 70-322 FROM N.A. (MYELOMA PROTEIN MOPC 21).  
 RX MEDLINE=8001837; PubMed=113776;  
 RA Rogers J., Clarke P., Salsner W.;  
 RT "Sequence analysis of cloned cDNA encoding part of an immunoglobulin  
 heavy chain.";

RL Nucleic Acids Res. 6:3305-3321(1979).  
 RN [4]  
 RP SEQUENCE (MYELOMA PROTEIN MOPC 21).  
 RX MEDLINE=78242288; PubMed=98524;  
 RA Adetungbo K.;  
 RT "Evolution of immunoglobulin subclasses. Primary structure of a  
 RT murine myeloma gamma1 chain.";  
 RL J. Biol. Chem. 253:6068-6075(1978).  
 RN [5]  
 RP DISULFIDE BONDS (MOPC 21).  
 RX MEDLINE=73008889; PubMed=5073237;  
 RA Svasti J., Milstein C.;  
 RT "The disulphide bridges of a mouse immunoglobulin G1 protein.";  
 RL Biochem. J. 126:837-850(1972).  
 CC - SUBCELLULAR LOCATION: Secreted.  
 CC - ALTERNATIVE PRODUCTS:  
 CC Event-Alternative splicing; Named isoforms=2;  
 CC Name=Secreted;  
 CC IsoId=P01868-1; Sequence=Displayed;  
 CC Note=May be the major isoform;  
 CC Name=Membrane-bound;  
 CC IsoId=P01869-1; Sequence=External;  
 CC -----  
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 CC -----  
 CC EMBL: V00793; CAA24172.1; -  
 CC EMBL: V00793; CAA24173.1; -  
 CC EMBL: V00793; CAA24174.1; -  
 CC EMBL: V00793; CAA24175.1; -  
 CC EMBL: V00793; CAA24176.1; -  
 CC PIR: A02159; G1MS.  
 CC PDB: 1IGC; 03-JUN-95.  
 DR GLCOSuitedB; P01868; -  
 DR MGD; MGI:96446; 1gh-4.  
 DR InterPro: IPR007110; Ig-1-like.  
 DR InterPro: IPR003597; Ig\_c1.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR Pfam: PF00047; Ig\_3.  
 DR SMART; SM00407; IGc1\_2.  
 DR SMART; SM00407; IGc1\_2.  
 DR PROSITE; PS00835; IG-LIKE; 3.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;  
 KW Alternative splicing; 3D-structure.  
 FT NON\_TER 1 1  
 FT DOMAIN 1 97 CH1.  
 FT DOMAIN 98 110 HINGE.  
 FT DOMAIN 111 217 CH2.  
 FT DOMAIN 218 324 CH3.  
 FT DISULFID 27 82  
 FT DISULFID 102 102 INTERCHAIN (WITH A LIGHT CHAIN).  
 FT DISULFID 104 104 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 138 198  
 FT CARBOHYD 174 174  
 FT DISULFID 244 302 N-LINKED (GLCNAC. . .).  
 FT MOD\_RES 324 324 /FTID=CAR\_000055.  
 FT CONFLICT 276 276 REMOVED POST-TRANSLATIONALLY.  
 FT CONFLICT 278 278 N -> D (IN REF. 3).  
 SO SEQUENCE 324 AA; 35704 MW; A338812F3D1FC93 CRC64;  
 Query Match 45.5%; Score 1145; DB 1; Length 324;  
 Best Local Similarity 62.3%; Pred. No. 1.5e-71;  
 Matches 207; Conservative 55; Mismatches 60; Indels 10; Gaps 4;  
 QY 145 ASTKGPVPLAPSSSTSGGTALCLVNDYFPEPVTVSWNSGALTSGVHTPPAVLQSS 204

ID	GCB_RAT	STANDARD:	PRT:	333 AA.
AC	P20761;			
DY	01-FEB-1991 (Rel. 17, Created)			
DY	01-FEB-1991 (Rel. 17, Last sequence update)			
DY	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Ig gamma-2B chain C region.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.			
OX	NCBI_Taxid=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RK	MEDLINE=89232738; PubMed=3149946;			
RA	Bueggemann M.;			
RT	"Evolution of the rat immunoglobulin gamma heavy-chain gene family.";			
RL	Gene 74:473-483(1988).			
CC	- - SIMILARITY: Contains 3 immunoglobulin-like domains.			
DR	HSSP; PS0018; PS0018.			
DR	HSSP; P01842; 7FAB.			
DR	InterPro; IPR007110; Ig-I like.			
DR	InterPro; IPR003597; Ig_cI.			
DR	InterPro; IPR003006; Ig_MHC.			
DR	Pfam; PF00047; Iq_3.			
DR	SMART; SM00407; IGc1. 2.			
DR	PROSITE; PS50835; IG_LIKE; 3.			
KW	PROSITE; PS00290; IG_MHC; 1.			
KW	Immunoglobulin domain; Immunoglobulin C region; Repeat.			
FT	NON TER	1	1	
FT	DOMAIN	6	96	
FT	DOMAIN	124	223	
FT	DOMAIN	232	328	
FT	DISULFID	15	15	
FT	DISULFID	27	80	
FT	DISULFID	106	106	
FT	DISULFID	109	109	
FT	DISULFID	112	112	
FT	DISULFID	115	115	
FT	DISULFID	147	207	
FT	DISULFID	253	311	
SQ	SEQUENCE	333 AA;	36497 MW;	55FB64DA8D60A6 CMCK64;

Query Match                  45.5%; Score 1144.5; DB 1; Length 333;  
 Best local Similarity      63.7%; Pred. No. 1.7e-71;  
 Matches 214; Conservative 45; Mismatches 68; Indels 9; Gaps 3

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145 ASKTGVSVPPLAPSSKSISGGTALGCIVKYDFPEPTVSVNSGALTSGVHTPPAYLQS 204
      | ||| :|||::|||||   : | ||||| |||||:|||||:::|||||::| |||||::|
  
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CC	RESULT 11
CC	GCIM_MOUSE
CC	ID GCIM_MOUSE STANDARD; PRT; 393 AA.
AC	P01869;
DT	21-JUL-1986 (Rel. 01, Created)
DT	01-AUG-1991 (Rel. 19, Last sequence update)
DT	15-SEP-2003 (Rel. 42, Last annotation update)
DE	Ig gamma-1 chain C region, membrane-bound form.
OS	Mus musculus (Mouse).
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
CC	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=80045036; PubMed=115593;
RA	Honjo T., Odate M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
RA	Takahashi N., Mano Y.;
RT	"Cloning and complete nucleotide sequence of mouse immunoglobulin
RT	gamma 1 chain gene";
RL	Cell 18:559-568(1979).
RN	[2]
RP	SEQUENCE OF 323-393 FROM N.A.
RX	MEDLINE=82197626; PubMed=6804950;
RA	Tyler B.M., Cowman A.F., Gerodakis S.D., Adams J.M., Bernard O.;
RT	"RNA for surface immunoglobulin gamma chains encodes a highly
RT	conserved transmembrane sequence and a 28-residue intracellular
RT	domain";
RL	Proc. Natl. Acad. Sci. U.S.A. 79:2008-2012(1982).
RN	[3]
RP	SEQUENCE OF 323-366 FROM N.A.
RX	MEDLINE=82115295; PubMed=6799207;
RA	Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl M.,
RA	Eisenberg D., Wall R.;
RT	"Gene segments encoding transmembrane carboxyl termini of
RT	immunoglobulin gamma chains";
RL	Cell 26:19-27(1981).
RN	[4]
RP	SEQUENCE OF 1-44 FROM N.A.
RX	MEDLINE=82222190; PubMed=6283537;
RA	Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
RT	"Nucleotide sequences of gene segments encoding membrane domains of
RT	immunoglobulin gamma chains";
RL	Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
CC	-1- ALTERNATIVE PRODUCTS:
CC	Event=Alternative splicing; Named isoforms=2;
CC	Name=Membrane-bound;
CC	Isoid=P01869-1; Sequence=Displayed;
CC	Name=Secreted;
CC	Isoid=P01868-1; Sequence=External;
CC	Note=May be the major isoform;
CC	

```

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CC or send an email to license@isb-sib.ch).
CC -----
CC DR EMBL: V00793; CAA24172.1; -
CC DR EMBL: V00793; CAA24173.1; -
CC DR EMBL: V00793; CAA24174.1; -
CC PIR: B02159; G1MSM.
CC
CC PDB: 15C8; 23-MAR-99.
CC PDB: 1AE6; 18-MAR-98.
CC PDB: 1CL7; 12-JAN-00.
CC PDB: 1F11; 06-FEB-01.
CC PDB: 1F58; 29-DEC-99.
CC PDB: 1KCS; 24-JUL-02.
CC PDB: 1KCR; 11-MAY-02.
CC PDB: 25C8; 09-JUL-99.
CC MGD: MGI:96446; Igh-4.
CC DR Interpro: IPR007110; Ig-like.
CC DR Interpro: IPR003597; Ig-cl.
CC DR Interpro: IPR003006; Ig_MHC.
CC DR Pfam: PF00047; Ig; 3.
CC DR SMART: SM00407; IGc1; 2.
CC DR PROSITE: PS00835; IG-LIKE; 3.
CC DR PROSITE: PS00290; IG_MHC; 1.
CC KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
CC Alternative splicing; Transmembrane; 3D-structure.
CC
CC FT NON_TER 1 1
CC FT DOMAIN 1 97 CH1.
CC FT DOMAIN 98 110 HINGE.
CC FT DOMAIN 111 217 CH2.
CC FT DOMAIN 218 324 CH3.
CC
CC FT DISULFID 27 82
CC FT DISULFID 102 102 INTERCHAIN (WITH A LIGHT CHAIN).
CC FT DISULFID 104 104 INTERCHAIN (WITH A HEAVY CHAIN).
CC FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
CC FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
CC FT DISULFID 138 198
CC FT CARBOHYD 174 174 N-LINKED (GLCNAC. . .).
CC FT TRANSMEM 244 302
CC FT TRANSMEM 340 357
CC FT DOMAIN 358 393 POTENTIAL.
CC SEQUENCE 393 AA; 43386 MW; 4CC88343B7A1CE27 CRC64;
CC
CC Query Match 45.3%; Score 1140; DB 1; Length 393;
CC Best Local Similarity 62.2%; Pred. No. 4.3e-71;
CC Matches 206; Conservative 55; Mismatches 60; Indels 10; Gaps 4;
CC
CC QY 145 ASTGSPVPLAPSSKSGGTAALGCLVKDYFPEPVVSWNSGALTSGVHPFPAVLOSS 204
CC DB 1 AKTTPPSVPLAPSAAGTSMVTLGCLVKGFPEPVVWNSGSLSSGVHPFPAVLOSD 60
CC
CC QY 205 GLVSLSVVTPSSSLGTQTYICNVNHRPSTKTVKREPKSCDTHTCPP--CPAPEL 262
CC DB 61 -LYTLSSSVTVPSRPSELYTCNVNHRPSTKTVKREPKSCDTHTCPP--CPAPEL 114
CC
CC QY 263 GGPVSELPKPKDTLMSKRPVEYTCVVDVSHEDPEVKFMVYVDGVEVHNKTRPREQ 322
CC DB 115 --SSVFIPPKPKDVLITLTPKVCVVDVSKDDEVOFSWFDVDEVHFGQTPREBO 172
CC
CC QY 323 YNSGTVRVSVTLVHODVNLGKEVKCKAKSKNALPARIKITSKANGQREPOVYTLPSR 382
CC DB 173 FNSFTRSVSELPIMHODVNLGKEVKCKAKSKNALPARIKITSKANGQREPOVYTLPSR 232
CC
CC QY 383 EEMKKNQVSLTCLVGYFPDIAVEMSGNPENNYKTPPYLDGSGFFSLKTLVKS 442
CC DB 233 EQMAKDKVSLCMITDFEPEDITYEMONGQPAEYKTKQTPIMNTNGSFYSLKLVKS 292
CC
CC QY 443 RMQGGNVFSCVMHEALHNHYTKSLSLSPG 473

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DB 293 NMEAGNFTCSVLHGLHNHTEKSLSPG 323
DB
DB RESULT 12
DB GC3M_MOUSE STANDARD; PRT; 398 AA.
DB ID GC3M_MOUSE
DB AC P03987;
DB DT 23-OCT-1986 (rel. 02, Created)
DB DT 01-AUG-1991 (rel. 19, Last sequence update)
DB DT 15-JUL-1999 (rel. 38, Last annotation update)
DB DE Ig gamma-3 chain C region, membrane-bound form.
DB OS Mus musculus (Mouse).
DB OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
DB OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
DB OX NCBI_TaxID=10090;
DB
DB RP SEQUENCE FROM N.A.
DB RX MEDLINE=85027161; PubMed=6092053;
DB RA Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
DB RA Tucker P.W., Blattner F.R.;
DB RT "Structural analysis of the murine IgG3 constant region gene.";
DB RL EMBO J. 3:2041-2046(1984).
DB
DB RN [2]
DB RP SEQUENCE OF 328-398 FROM N.A.
DB RX MEDLINE=84041483; PubMed=6314258;
DB RA Komaromy M., Clayton L., Rogers J., Robertson S., Ketman J.,
DB RA Wall R.;
DB RT "The structure of the mouse immunoglobulin in gamma 3 membrane gene
DB RT segment.";
DB RL Nucleic Acids Res. 11:6775-6785(1983).
DB
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DB CC -----
DB CC DR EMBL: J00451; AAB59655.1; -
DB CC DR EMBL: V01526; CAA24767.1; ALT_SEQ.
DB CC DR PIR: A02156; G3MSM.
DB CC DR HSP: P01857; 1FC1.
DB CC DR Interpro: IPR007110; Ig-like.
DB CC DR Interpro: IPR003597; Ig-cl.
DB CC DR Interpro: IPR003006; Ig_MHC.
DB CC DR Pfam: PF00047; Ig; 3.
DB CC DR SMART: SM00407; IGc1; 2.
DB CC DR PROSITE: PS00835; IG-LIKE; 3.
DB CC DR PROSITE: PS00290; IG_MHC; 1.
DB CC KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
DB CC Transmembrane; Alternative splicing.
DB CC
DB CC FT NON_TER 1 1
DB CC FT DOMAIN 1 97 CH1.
DB CC FT DOMAIN 98 113 HINGE.
DB CC FT DOMAIN 114 223 CH2.
DB CC FT DOMAIN 224 327 CH3.
DB CC FT TRANSMEM 346 362
DB CC FT DOMAIN 363 398 POTENTIAL.
DB CC FT DOMAIN 398 398 CYTOPLASMIC (POTENTIAL).
DB CC FT CONFLICT 342 342 E -> G (IN REF. 2).
DB CC FT CONFLICT 342 342 E -> Q (IN REF. 2).
DB CC FT CONFLICT 388 388 P -> F (IN REF. 2).
DB CC SEQUENCE 398 AA; 43929 MW; CFF264B50A41B95 CRC64;
DB
DB Query Match 45.3%; Score 1139; DB 1; Length 398;
DB Best Local Similarity 64.7%; Pred. No. 5.1e-71;
DB Matches 213; Conservative 44; Mismatches 68; Indels 4; Gaps 3;
DB
DB QY 146 STGSPVPLAPSSKSGGTAALGCLVKDYFPEPVVSWNSGALTSGVHPFPAVLOSS 205
DB DB 1 TTPAPSVPLAPGCSDTSGSSVTLGCLVKGFPEPVVWNSGSLSSGVHPFPAVLO-SG 59

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CC		-----
DR	EMBL; V00798; CAA24178.1; .	
DR	PIR; A02152; GZMSA.	
DR	PDB; 1E4W; 12-JUL-01.	
DR	PDB; 1E4X; 12-JUL-01.	
DR	PDB; 1MNU; 06-MAY-99.	
DR	InterPro: IPR007110; Ig-like.	
DR	InterPro: IPR003597; Ig-cl.	
DR	InterPro: IPR003006; Ig_MHC.	
DR	pfam; PF00047; Ig_2.	
DR	SMART; SM00407; IGcl; 2.	
DR	PROSITE; PS50835; IG-LIKE; 3.	
DR	PROSITE; PS00290; IG_MHC; 1.	
KW	Immunoglobulin domain; Immunoglobulin C region; 3D-structure; Repeat.	
FT	NON_TER	1
FT	DOMAIN	6 98 IG-LIKE 1.
FT	DOMAIN	121 220 IG-LIKE 2.
FT	DOMAIN	229 325 IG-LIKE 3.
FT	DISULFID	15 15 INTERCHAIN (WITH A LIGHT CHAIN) .
FT	DISULFID	27 82 INTERCHAIN (WITH A HEAVY CHAIN) .
FT	DISULFID	107 107 INTERCHAIN (WITH A HEAVY CHAIN) .
FT	DISULFID	110 110 INTERCHAIN (WITH A HEAVY CHAIN) .
FT	DISULFID	112 112 INTERCHAIN (WITH A HEAVY CHAIN) .
FT	DISULFID	144 204
FT	DISULFID	250 308
FT	MOD_RES	330 330
SO	SEQUENCE	330 AA; 36389 MW; B64361C5445A6864 (RC64); REMOVED POST-TRANSLATIONALLY.
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Query Match	Best Local Similarity	44.9%; Score 1129; DB 1: Length 330;
Matches 212; Conservative	43; Mismatches 73; Indels 4; Gaps 3,	
QY	145 ASTKGPVFLPAPSKSRSGGTALGCIYKRYFPPEPVIVIMNSGLTSGVHTFPAYLDSS	204
DB	1 AKTTAPSVYPLPACGGDTGSSVTLCGLCYRKFPPEPYVLINMSGSLSGVHTFPAYLDSD	60
QY	205 GLYLSSVYVPSSSLGTGYICNVNHNKPSMTKYDKRAYEKSCDTHTCPP--CPAPELL	262
DB	61 -LYTLSSVYLTSTSTWSPQSITTCNVANHAASSTRKDKE?KG-PTRKCPROCKCAPML	118
QY	263 GGPSVFLEPPPKDKTLMISRTPEYTCVVVDVSHEDPEVKIMNYDVGEVNNAKTTPREEQ	322
DB	119 GGPSVFLEPPPKIKDIVLMISTSPIVTCVVVDVSEDDPDQVLSMFVNNEVHQAQTRED	178
QY	323 YNSTRYRVSVLTVALHOMLNKEKKYCKSNKALPARIEKLTISKAKGQREPOVYTLPSRS	382
DB	179 YNSTLRVVSALPIQHDMWSKERKCYKNNDLPAPIERTISKPGSVRAQVYVLPPE	238
QY	383 EEMKRNQVSLCLVKGFFPSDIAVEWESNGOPENNYKTTPELDSGSEFFLYSKLTVKS	442
DB	239 EEMKRVQTYTLCTMDTFMRDEIYYEMTNNGKITELNYKTEPYLDSGSIYFMYSKLVEKK	298
QY	443 RMQGQNFSCVMHEALNNHYTKSLSLSPGK	474
DB	299 NMVERNSYSCSVVHEGLNHHTHTKSFRTPGK	330
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RESULT 14	GCC_RAT	
ID	GCC_RAT	STANDARD; PRT; 329 AA.
AC	P20762;	
DT	01-FEB-1991 (Rel. 17, Created)	
DT	01-FEB-1991 (Rel. 17, Last sequence update)	
DT	15-JUL-1999 (Rel. 38, Last annotation update)	
DE	Ig gamma-2C chain C region. Rattus norvegicus (Rat).	

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP MEDLINE=88166903; PubMed=3127222;
RX Bruggemann M., Delmastro-Galile P., Walzmann H., Calabi F.;
RA "Sequence of a rat immunoglobulin gamma 2c heavy chain constant
RT region cDNA: extensive homology to mouse gamma 3."
RL Eur. J. Immunol. 18:317-319(1988).
CC -----
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CC -----
CC EMBL, X07189; CAA30169.1; -.
DR PIR: S00847; S00847.
DR HSP: P01842; 7PAB.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003587; Ig_C1.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig; 2.
DR SMART: SM00407; IgC1; 2.
DR PROSITE: PS50835; IG-LIKE; 3.
DR PROSITE: PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1 1
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 113 HINGE.
FT DOMAIN 114 222 H2.
FT DOMAIN 223 329 CH3.
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 82 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 111 111 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 113 113 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 143 203
FT DISULFID 249 307
SQ SEQUENCE 329 AA: 36571 MW: 5FCD7B7933850773 CRC64;

Query Match 44.8%; Score 1127.5; DB 1; Length 329;
Best Local Similarity 62.8%; Pred. No. 2.5e-70;
Matches 209; Conservative 51; Mismatches 66; Indels 7; Gaps 3;

QY 145 ASTKGPVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVYVSNMNGALITSGVHTFPVAVLOSS 204
DB 1 AATTAPSVYPLVPGGSGTSGSLVLTGCLVKGYFPEPVYVKNMNGALSSGVHTFPVAVLO-S 59
QY 205 GLYSLSVVTVPSSSLGTQTYICNVNHRKPSNTKVKRREPKSCDTHNCP--CPAPEL 261
DB 60 GLYTLSSSVTVSSSTWSSQYVCSVAHPATKSNLKRLEPR---RPKRPFPDIDSCDDN 116
QY 262 LGPSVLEFPKPKDLMISRTPEVTVVVDVSHDEPEVKFMYVDGVEVNAKTKPREE 321
DB 117 LGRPVVFTEPPKPKDILMITLTPKVTGVVDVSEEPDQVFMFVDNVAVFPAQIQPHBE 176
QY 322 QYNSTVRYVSVLTVAHOMLNKEKCKVSKNKAAPLEKTSKAKGQPREQVYTPPSS 381
DB 177 QLNGETFRVSTLTIHODMWSGKEPKCKVNNKDLSPLEKTSKRGAKRTQVYTPP 236
QY 382 REEMTKNOVSLTCLVKGYFSPDAVEMESNGOPENNNYKTPPVLDSDGSFFLYSKLTVDK 441
DB 237 RQOMKKNVSLTCLVMTSTFPAISYEMERNGELLEDYKNTLPVLDSDGSFFLYSKLSDVT 296
QY 442 SRMOGVNFSQSVHMEALHNHYTQKSLSLSPCK 474
DB 297 DSMRGDIYTCVSVAHEALHNHHTQKLSRSPCK 329

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GCAB_MOUSE
ID GCAB_MOUSE STANDARD; PRT; 335 AA.
AC P01664;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig gamma-2a chain C region secreted form (B allele).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6;
RC MEDLINE=82037861; PubMed=6170065;
RA Schreier P.H., Bothwell A.L.M., Mueller-Hill B., Baltimore D.;
RT "Multiple differences between the nucleic acid sequences of the
RT Ig2a and Ig2ab alleles of the mouse."
RL Proc. Natl. Acad. Sci. U.S.A. 78:4495-4499(1981).
RN [2]
RP SEQUENCE.
RX MEDLINE=82037777; PubMed=6794027;
RA Dognin M.J., Lauwereys M., Strosberg A.D.;
RT "Multiple amino acid substitutions between murine gamma 2a heavy
RT chain C regions of Ig1a and Ig1b alleotypic forms."
RL Proc. Natl. Acad. Sci. U.S.A. 78:4031-4035(1981).
CC -1- SUBCELLULAR LOCATION: Secreted (Potential).
CC -1- ALTERNATIVE PRODUCTS.
CC Event-Alternative splicing; Named isoforms=2;
CC Name-Secreted;
CC IsoId=P01864-1; Sequence=Displayed;
CC Note-Probably the major isoform;
CC Name-Membrane-bound;
CC IsoId=P01865-1; Sequence=External;
CC -1- MISCELLANEOUS: THE SEQUENCE DIFFERS FROM THAT OF THE A ALLELE,
CC FROM BALB/C MICE, AT 15 OF THE POSITIONS.
CC -1- SIMILARITY: Contains 3 immunoglobulin-like domains.
CC -----
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CC -----
CC EMBL, J00479; -. NOT_ANNOTATED_CDS.
DR PIR: A02153; G2MSAB.
DR PDB: 1B0G; 23-MAR-99.
DR PDB: 1HH6; 26-JAN-01.
DR PDB: 1HH9; 12-JAN-01.
DR PDB: 1HI6; 08-FEB-01.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003587; Ig_C1.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig; 3.
DR SMART: SM00407; IgC1; 2.
DR PROSITE: PS50835; IG-LIKE; 3.
DR PROSITE: PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Alternative splicing;
KW 3D-structure; Repeat.
FT NON_TER 1 1
FT DOMAIN 1 98 IG-LIKE 1.
FT DOMAIN 126 225 IG-LIKE 2.
FT DOMAIN 234 330 IG-LIKE 3.
SQ SEQUENCE 335 AA: 36596 MW: FA33827920BB13C6 CRC64;

Query Match 44.8%; Score 1126.5; DB 1; Length 335;
Best Local Similarity 61.6%; Pred. No. 2.9e-70;
Matches 207; Conservative 52; Mismatches 70; Indels 7; Gaps 2;

QY 145 ASTKGPVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVYVSNMNGALITSGVHTFPVAVLOSS 204

```

```
Db      1 AKTAAPSVYPLVPCGGTTGSSSVTLGCLVKGYPPEPVTLTWNSGSLSGVHTFPALLQ-S 59
QY      205 GLYSLSSVYTVPSSSLSIGTOTYTCNVNHRKSNTRKVDKRVEPK-----SCDKTHTCPPCA 258
        |||:||| ||| :|: ||| | :|:|||:|:| | ||| |
Db      60 GLYTLSSSVYTVSNTPSQITICNVNHPASSSTRKVDKIEPRVPITONPCPPHQRVPPCAA 119
        |||:||| ||| :|: ||| | :|:|||:|:| | ||| |
QY      259 PELLGAPSVFELPPPKPKDTLMSRPEPEVCVVVDVSHEDPEVKFNNYVDGVEVHNAKTKP 318
        |:|||:||| ||| ||| ||| :|:||| ||| :|:|: ||| :|:|:
Db      120 PLLLGAPSVFIFPPKIKDYLMLISLSPMTCVVVDVSEDDPDVQISNFWNNVEVHTAQTOT 179
        |||:||| ||| ||| ||| :|:||| ||| :|:|: ||| :|:|:
QY      319 REEOYNSYRYRVSVLTVLHQDMLNKEKYCKVSNKALPAPIEKTISKAKGQPREPOVYTL 378
        | ||| ||| | :|:|: ||| :|:||| ||| :|:||| ||| :|:||| |
Db      180 HREDYNSYRYRVSVLTVLHQDMLNKEKYCKVSNKALPAPIEKTISKAKGQPREPOVYTL 239
        |||:||| ||| ||| ||| :|:||| ||| :|:||| ||| :|:||| |
QY      379 PPSREEMTKNOVSLTCLVKGYPSPDIAVEMESNGQPENNYKTTTPVLDSDGSFELYSKLT 438
        || |||| : ||||: | :|:|||: ||| | ||| ||| :|:||| |
Db      240 PPPAEEMTKKEPSLTCMITGFLPAELIAYDMTISNGRTEONYKNTATVLDSDGSYFMYSKLR 299
        || |||| : ||||: | :|:|||: ||| | ||| ||| :|:||| |
QY      439 VDKSRMOQGNVFCSVMHPEALHNHYTQKSLSLSPGK 474
        | || :|:|: ||| ||| ||| :|:||| ||| :|:||| ||| :|:||| |
Db      300 VOKSTWERSLFCACSVHVEVLHNHLTKTISRSLGK 335
        || || :|:|: ||| ||| ||| :|:||| ||| :|:||| ||| :|:||| |
```

Search completed: September 12, 2003, 13:01:15  
Job time : 21.0847 secs

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